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OM protein - protein search, using sw model

Run on: March 5, 2005, 17:43:36 ; Search time 43 Seconds  
(without alignments)  
430.534 Million cell updates/sec

**Title:** US-10-006-856A-194

Perfect score:

Sequence: 1 MGLSIFLLLCVLGLSQAATP.....GVITYICKYVDWIRMIMRNN 248

Scoring table: BLOSUM62

Scoring table:  $\text{Gapop } 10.0$  ,  $\text{Gapext } 0.5$

Searched: 513545 beqs, 74649064 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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post-processing: Minimum Match 0%

Post-processing: Minimum Match 0% Maximum Match 100%

Maximum Match 100%  
Listing first 1500 summaries

Database : Issued Patents AA:\*

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6: /cgn2\_6/ptodata/1/iaa/backfiles1.pcp:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query		Length	DB	ID	Description
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1	1359.5	98.9	7	249	4	US-09-949-016-8151	Sequence 8151, Ap
2	1301	94.7	254	4	US-09-949-016-6948	Sequence 6948, Ap	
3	811	59.0	162	4	US-09-244-111-6	Sequence 6, Appli	
4	630.5	45.9	260	4	US-09-618-259-7	Sequence 7, Appli	
5	626.5	45.6	260	3	US-09-070-526-2	Sequence 2, Appli	
6	622.5	45.3	260	3	US-09-025-059-3	Sequence 3, Appli	
7	622.5	45.3	260	3	US-09-028-271A-7	Sequence 7, Appli	
8	622.5	45.3	260	4	US-09-618-259-8	Sequence 8, Appli	
9	618.5	45.0	250	4	US-09-205-258-427	Sequence 427, App	
10	618.5	45.0	282	3	US-09-025-059-1	Sequence 1, Appli	
11	602.5	43.9	288	4	US-09-386-642-13	Sequence 13, Appl	
12	598.5	43.6	289	4	US-09-386-642-14	Sequence 14, Appl	
13	597.5	43.5	248	3	US-08-944-483-24	Sequence 24, Appl	
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15	567	41.3	290	4	US-09-949-016-8166	Sequence 8166, Ap	
16	564.5	41.1	270	4	US-09-949-016-7712	Sequence 7712, Ap	
17	564.5	41.1	293	4	US-09-509-908-2	Sequence 2, Appli	
18	564	41.0	276	1	US-08-467-155A-1	Sequence 1, Appli	
19	564	41.0	276	2	US-08-628-198-1	Sequence 1, Appli	
20	564	41.0	276	3	US-09-201-038-1	Sequence 1, Appli	
21	564	41.0	325	5	PCF-US96-07343-1	Sequence 1, Appli	
22	563	41.0	325	4	US-09-949-016-7713	Sequence 7713, Ap	
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102	494	36.0	254	4	US-09-679-426-523	Sequence 523, App	175	458	33.3	228	2	US-08-801-499-7	Sequence 7, Appli
103	494	36.0	254	4	US-09-759-143-523	Sequence 523, App	176	458	33.3	228	2	US-08-615-271-7	Sequence 7, Appli
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107	493	35.9	262	2	US-08-681-151-4	Sequence 4, Appli	180	458	33.3	228	3	US-09-106-466A-7	Sequence 7, Appli
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110	493	35.9	262	3	US-09-210-084-4	Sequence 4, Appli	183	457.5	33.3	237	3	US-08-767-820A-1	Sequence 1, Appli
111	493	35.9	262	3	US-09-478-957-4	Sequence 4, Appli	184	457.5	33.3	237	3	US-08-622-046B-7	Sequence 7, Appli
112	493	35.9	262	4	US-09-764-762-4	Sequence 4, Appli	185	457.5	33.3	237	3	US-08-944-483-38	Sequence 38, Appl
113	492	35.8	225	2	US-09-027-337-5	Sequence 5, Appli	186	457.5	33.3	237	3	US-08-100-264-3	Sequence 3, Appli
114	492	35.8	225	4	US-08-644-600-5	Sequence 5, Appli	187	457.5	33.3	237	4	US-09-303-339-2	Sequence 2, Appli
115	492	35.8	225	4	US-08-554-600A-5	Sequence 5, Appli	188	457.5	33.3	237	4	US-08-843-076D-7	Sequence 7, Appli
116	492	35.8	262	1	US-08-744-026-4	Sequence 4, Appli	189	457.5	33.3	237	4	US-09-303-208-1	Sequence 1, Appli
117	492	35.8	262	2	US-09-102-732-4	Sequence 4, Appli	190	455.5	33.2	237	1	US-08-096-946-11	Sequence 11, Appl
118	492	35.8	262	3	US-09-361-767-4	Sequence 4, Appli	191	455.5	33.2	237	5	PCT-US94-07329-11	Sequence 11, Appl
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121	487.5	35.5	449	4	US-09-636-215-617	Sequence 617, App	194	455.5	33.2	261	3	US-08-767-820A-19	Sequence 19, Appl
122	487.5	35.5	449	4	US-09-685-166A-617	Sequence 617, App	195	455.5	33.2	261	3	US-08-622-046B-3	Sequence 3, Appli
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124	487.5	35.5	449	4	US-09-759-143-617	Sequence 617, App	197	454.5	33.1	232	2	US-09-252-329-31	Sequence 31, Appl
125	487.5	35.5	449	4	US-09-651-236-617	Sequence 617, App	198	454.5	33.1	244	5	PCT-US95-06157-10	Sequence 10, Appl
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128	487	35.4	224	3	US-09-296-219-13	Sequence 13, Appl	201	452.5	32.9	244	3	US-08-767-820A-10	Sequence 10, Appl
129	478	34.8	224	3	US-08-944-483-35	Sequence 35, Appl	202	452.5	32.9	244	3	US-08-622-046B-16	Sequence 16, Appl
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131	472.5	34.4	220	3	US-09-352-616A-327	Sequence 327, App	204	452.5	32.9	244	4	US-08-843-076D-5	Sequence 2, Appli
132	472.5	34.4	220	4	US-09-232-149A-327	Sequence 327, App	205	450.5	32.8	237	2	US-08-844-024-2	Sequence 2, Appli
133	472.5	34.4	220	4	US-08-636-215-327	Sequence 327, App	206	450.5	32.8	237	3	US-08-718-547-2	Sequence 16, Appl
134	472.5	34.4	220	4	US-09-685-166A-327	Sequence 327, App	207	450.5	32.8	237	3	US-08-768-859A-16	Sequence 16, Appl
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136	472.5	34.4	220	4	US-09-679-426-327	Sequence 327, App	209	450.5	32.8	237	3	US-08-622-046B-12	Sequence 37, Appl
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145	470.5	34.2	261	4	US-08-907-402-1	Sequence 1, Appli	218	448.5	32.6	237	5	PCT-US94-07329-10	Sequence 10, Appl
146	470.5	34.2	261	4	US-09-618-259-10	Sequence 10, Appl	219	448.5	32.6	237	5	PCT-US95-06157-16	Sequence 16, Appl
147	470.5	34.2	261	4	US-09-618-259-10	Sequence 10, Appl	220	447.5	32.6	237	3	US-08-768-859A-16	Sequence 21, Appl
148	470.5	34.2	375	4	US-09-755-100A-11	Sequence 11, Appl	221	447.5	32.6	237	3	US-08-767-820A-21	Sequence 21, Appl
149	469.5	34.2	271	1	US-08-944-483-39	Sequence 39, Appl	222	447.5	32.6	237	3	US-08-622-046B-1	Sequence 1, Appli
150	469.5	34.2	271	2	US-08-467-155A-10	Sequence 10, Appl	223	447.5	32.6	237	3	US-09-100-264-12	Sequence 12, Appl
151	469.5	34.2	271	2	US-08-628-198-10	Sequence 10, Appl	224	447.5	32.6	237	4	US-08-843-076D-8	Sequence 8, Appli
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153	469	34.1	284	1	US-09-386-642-54	Sequence 54, Appl	226	445	32.4	240	5	PCT-US96-09303-1	Sequence 1, Appli
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161	459	33.4	262	4	US-09-755-100A-14	Sequence 14, Appl	234	426.5	31.0	205	3	US-09-439-313-176	Sequence 176, App
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163	458.5	33.4	261	3	US-08-767-820A-6	Sequence 6, Appli	236	426.5	31.0	205	4	US-09-232-149A-176	Sequence 176, App
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167	458.5	33.4	261	4	US-08-843-076D-3	Sequence 3, Appli	240	426.5	31.0	205	4	US-09-115-453-176	Sequence 176, App
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169	458	33.3	228	1	US-08-278-091-7	Sequence 7, Appli	242	426.5	31.0	205	4	US-09-679-426-176	Sequence 176, App
170	458	33.3	228	1	US-08-483-859-7	Sequence 7, Appli	243	426.5	31.0	205	4	US-09-759-143-176	Sequence 176, App
171	458	33.3	228	1	US-08-472-173-7	Sequence 7, Appli	244	426.5	31.0	205	4	US-09-651-236-176	Sequence 176, App
172	458	33.3	228	2	US-08-487-167-7	Sequence 7, Appli	245	418	30.4	207	4	US-09-244-111-4	Sequence 4, Appli
173	458	33.3	228	2	US-08-482-816-7	Sequence 7, Appli	246	417.5	30.4	233	2	US-08-738-413B-9	Sequence 9, Appli

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249	393	28.6	236	1	US-08-684-862-5	Sequence 5, Appl	322	354	25.8	461	6	5270178-18	Patent No. 5270178
250	389	28.3	235	2	US-08-738-413B-10	Sequence 10, Appl	323	353.5	25.7	230	3	US-08-944-483-62	Sequence 62, Appl
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252	387	28.2	253	6	5223425-8	Patent No. 5223425	325	353	25.7	274	2	US-08-978-404B-5	Sequence 5, Appl
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254	385	28.0	232	2	US-08-738-413B-11	Sequence 11, Appl	327	353	25.7	314	4	US-09-023-942A-6	Sequence 6, Appl
255	385	28.0	250	6	5223425-4	Patent No. 5223425	328	353	25.7	314	4	US-09-907-794A-257	Sequence 257, App
256	385	28.0	250	6	5223425-4	Patent No. 5223425	329	353	25.7	314	4	US-09-905-125A-257	Sequence 257, App
257	377.5	27.5	154	3	US-09-261-416-5	Sequence 5, Appl	330	353	25.7	314	4	US-09-902-775A-257	Sequence 257, App
258	374.5	27.3	238	6	5223425-5	Patent No. 5223425	331	353	25.7	314	4	US-09-906-700-257	Sequence 257, App
259	374.5	27.3	238	6	5223425-5	Patent No. 5223425	332	353	25.7	314	4	US-09-903-603A-257	Sequence 257, App
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262	374	27.2	260	6	5223425-10	Patent No. 5223425	335	353	25.7	314	4	US-09-905-381A-257	Sequence 257, App
263	374	27.2	260	6	5223425-10	Patent No. 5223425	336	353	25.7	314	4	US-09-906-618-257	Sequence 257, App
264	370.5	27.0	228	3	US-08-944-483-44	Sequence 44, Appl	337	351.5	25.6	814	1	US-08-750-711-1	Sequence 1, Appl
265	370	26.9	418	4	US-09-370-838-62	Sequence 62, Appl	338	349.5	25.4	166	4	US-09-636-215-838	Sequence 838, App
266	370	26.9	418	4	US-09-854-133-62	Sequence 62, Appl	339	349.5	25.4	166	4	US-09-685-166A-838	Sequence 838, App
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273	366	26.6	232	1	US-08-508-448C-19	Sequence 19, Appl	346	349	25.4	159	3	US-09-352-616A-172	Sequence 172, App
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284	364.5	26.5	400	3	US-08-749-699-33	Sequence 33, Appl	357	349	25.4	1019	2	US-08-596-405-4	Sequence 4, Appl
285	364.5	26.5	400	4	US-09-004-729-30	Sequence 30, Appl	358	349	25.4	1019	2	US-08-877-620-4	Sequence 4, Appl
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287	362.5	26.4	242	3	US-09-004-731-36	Sequence 36, Appl	360	349	25.4	1019	4	US-09-626-795-4	Sequence 4, Appl
288	362.5	26.4	242	3	US-08-749-699-36	Sequence 36, Appl	361	349	25.4	1083	1	US-08-296-014A-2	Sequence 2, Appl
289	362.5	26.4	242	4	US-09-004-729-36	Sequence 36, Appl	362	349	25.4	1083	2	US-08-596-405-2	Sequence 2, Appl
290	362.5	26.4	319	4	US-09-386-642-12	Sequence 12, Appl	363	349	25.4	1083	2	US-08-877-620-2	Sequence 2, Appl
291	362.5	26.4	328	4	US-09-386-642-11	Sequence 11, Appl	364	349	25.4	1083	4	US-09-287-368-2	Sequence 2, Appl
292	361.5	26.3	387	3	US-09-032-215-8	Sequence 8, Appl	365	349	25.4	1083	4	US-09-626-795-2	Sequence 2, Appl
293	361.5	26.3	387	3	US-09-032-215-13	Sequence 13, Appl	366	348	25.3	461	6	5460953-3	Patent No. 5460953
294	361	26.3	236	1	US-08-684-862-4	Sequence 4, Appl	367	348	25.3	461	6	5460953-3	Patent No. 5460953
295	360.5	26.2	299	3	US-08-944-483-66	Sequence 66, Appl	368	347	25.3	262	1	US-07-720-189-1	Sequence 1, Appl
296	358.5	26.1	232	4	US-09-959-392-31	Sequence 31, Appl	369	347	25.3	356	4	US-09-054-272-18	Sequence 18, Appl
297	358	26.1	812	4	US-08-991-761A-7	Sequence 7, Appl	370	347	25.3	409	3	US-09-065-872-2	Sequence 2, Appl
298	357.5	26.0	232	3	US-08-906-769-81	Sequence 81, Appl	371	347	25.3	409	4	US-09-667-570A-2	Sequence 2, Appl
299	357.5	26.0	232	3	US-08-906-616-81	Sequence 81, Appl	372	347	25.3	410	3	US-09-065-872-1	Sequence 1, Appl
300	357.5	26.0	232	3	US-08-817-795-81	Sequence 81, Appl	373	347	25.3	410	4	US-09-667-570A-1	Sequence 1, Appl
301	357.5	26.0	232	3	US-08-639-075A-81	Sequence 81, Appl	374	347	25.3	419	1	US-08-295-411-1	Sequence 1, Appl
302	357.5	26.0	232	3	US-09-012-431-81	Sequence 81, Appl	375	347	25.3	419	2	US-08-955-471-1	Sequence 1, Appl
303	357.5	26.0	232	3	US-09-012-692-81	Sequence 81, Appl	376	347	25.3	419	4	US-09-667-570A-3	Sequence 3, Appl
304	357.5	26.0	232	3	US-08-906-613-81	Sequence 81, Appl	377	347	25.3	419	4	US-10-182-263-1	Sequence 1, Appl
305	357.5	26.0	232	5	PCT-US95-14442A-81	Sequence 81, Appl	378	347	25.3	419	5	PCT-US92-10242-1	Sequence 1, Appl
306	357	26.0	268	4	US-09-949-016-10712	Sequence 10712, A	379	347	25.3	460	2	US-09-667-570A-1	Sequence 1, Appl
307	356.5	25.9	248	3	US-08-944-483-63	Sequence 63, Appl	380	347	25.3	460	2	US-08-756-506-4	Sequence 4, Appl
308	355.5	25.9	148	4	US-09-618-259-2	Sequence 2, Appl	381	347	25.3	461	4	US-08-756-506-2	Sequence 2, Appl
309	355.5	25.9	231	2	US-09-027-337-6	Sequence 6, Appl	382	347	25.3	461	4	US-10-182-263-2	Sequence 2, Appl
310	355.5	25.9	231	4	US-09-644-600-6	Sequence 6, Appl	383	347	25.3	461	4	US-09-054-272-32	Sequence 32, Appl
311	355.5	25.9	231	4	US-09-654-600A-6	Sequence 6, Appl	384	347	25.3	461	4	US-09-949-016-5921	Sequence 5921, Ap
312	355.5	25.9	276	2	US-09-016-366A-15	Sequence 15, Appl	385	347	25.3	461	6	5225537-2	Patent No. 5225537
313	355.5	25.9	276	2	US-08-978-404B-21	Sequence 21, Appl	386	347	25.3	485	4	5225537-2	Patent No. 5225537
314	354.5	25.8	461	6	5270178-2	Patent No. 5270178	387	346.5	25.2	791	1	US-09-949-016-10882	Sequence 1, Appl
315	354.5	25.8	461	6	5270178-2	Patent No. 5270178	388	346.5	25.2	791	3	US-08-643-219-1	Sequence 1, Appl
316	354	25.8	229	2	US-08-557-146-13	Sequence 13, Appl	389	346	25.2	234	3	US-08-851-350-1	Sequence 1, Appl
317	354	25.8	229	2	US-08-154-344-13	Sequence 13, Appl	390	346	25.2	241	3	US-08-944-483-46	Sequence 46, Appl
318	354	25.8	312	4	US-09-023-942A-4	Sequence 4, Appl	391	346	25.2	419	4	US-08-944-483-59	Sequence 59, Appl
319	354	25.8	461	6	5270178-17	Patent No. 5270178	392	346	25.2	419	4	US-10-182-263-5	Sequence 5, Appl

393	345.5	25.1	248	3	US-08-906-769-111	Sequence 111, App	466	339.5	24.7	253	3	US-09-578-303-4	Sequence 4, Appli
394	345.5	25.1	248	3	US-08-906-616-111	Sequence 111, App	467	339.5	24.7	258	1	US-07-990-301A-2	Sequence 2, Appli
395	345.5	25.1	248	3	US-08-817-795-111	Sequence 111, App	468	339.5	24.7	333	4	US-08-991-761A-8	Sequence 8, Appli
396	345.5	25.1	248	3	US-08-639-075A-111	Sequence 111, App	469	339	24.7	419	4	US-10-182-263-4	Sequence 4, Appli
397	345.5	25.1	248	3	US-09-012-431-111	Sequence 111, App	470	339	24.7	461	3	US-08-742-877-2	Sequence 2, Appli
398	345.5	25.1	248	3	US-09-012-692-111	Sequence 111, App	471	339	24.7	461	3	US-09-053-871A-21	Sequence 21, Appli
399	345.5	25.1	248	3	US-08-906-613-111	Sequence 111, App	472	339	24.7	461	6	US-10-133-907-5	Sequence 5, Appli
400	345.5	25.1	248	5	PCT-US95-1444A-111	Sequence 111, App	473	339	24.7	461	6	5521070-2	Patent No. 5521070
401	344	25.0	274	2	US-09-016-366A-21	Sequence 21, Appl	474	339	24.7	461	6	5521070-2	Patent No. 5521070
402	344	25.0	274	2	US-08-978-404B-16	Sequence 16, Appl	475	339	24.7	480	4	US-09-949-016-11123	Sequence 11123, A
403	343.5	25.0	273	2	US-08-978-404B-3	Sequence 3, Appli	476	339	24.7	481	4	US-09-949-016-9238	Sequence 9238, Ap
404	343.5	25.0	460	6	5270178-13	Patent No. 5270178	477	339	24.7	481	4	US-09-949-016-9239	Sequence 9239, Ap
405	343.5	25.0	460	6	5270178-14	Patent No. 5270178	478	339	24.7	637	4	US-09-949-016-11538	Sequence 11538, A
406	343.5	25.0	460	6	5270178-15	Patent No. 5270178	479	339	24.7	637	4	US-09-949-016-11539	Sequence 11539, A
407	343.5	25.0	460	6	5270178-16	Patent No. 5270178	480	338.5	24.6	230	1	US-08-379-621-2	Sequence 2, Appli
408	343.5	25.0	460	6	5270178-17	Patent No. 5270178	481	338.5	24.6	230	1	US-08-147-000B-2	Sequence 2, Appli
409	343.5	25.0	460	6	5270178-18	Patent No. 5270178	482	338.5	24.6	230	1	US-08-147-000B-2	Sequence 2, Appli
410	343.5	25.0	460	6	5270178-19	Patent No. 5270178	483	338.5	24.6	261	6	5270178-5	Patent No. 5270178
411	343.5	25.0	460	6	5270178-16	Patent No. 5270178	484	338.5	24.6	261	6	5270178-5	Patent No. 5270178
412	343	25.0	284	4	US-09-387-375-7	Sequence 7, Appli	485	338.5	24.6	308	3	US-08-705-875A-10	Sequence 10, Appl
413	343	25.0	284	4	US-10-041-400A-7	Sequence 7, Appli	486	338.5	24.6	308	4	US-09-242-999-10	Sequence 10, Appl
414	343	25.0	284	4	US-10-042-091A-7	Sequence 7, Appli	487	338	24.6	308	4	US-09-242-999-10	Sequence 10, Appl
415	342.5	24.9	248	3	US-09-032-215-37	Sequence 37, Appl	488	337.5	24.6	250	3	US-08-944-483-51	Sequence 51, Appl
416	342.5	24.9	249	3	US-09-032-215-37	Sequence 5, Appli	489	337	24.5	267	4	US-09-949-016-10711	Sequence 10711, A
417	342.5	24.9	273	2	US-08-978-404B-6	Sequence 6, Appli	490	337	24.5	235	3	US-08-944-483-48	Sequence 48, Appl
418	342.5	24.9	546	6	5200340-6	Patent No. 5200340	491	337	24.5	406	4	US-09-851-588-6	Sequence 6, Appli
419	342.5	24.9	546	6	5200340-6	Patent No. 5200340	492	337	24.5	435	4	US-09-607-745-2	Sequence 2, Appli
420	342.5	24.9	713	4	US-09-949-016-9983	Sequence 9983, Ap	493	337	24.5	437	4	US-09-851-588-8	Sequence 8, Appli
421	342.5	24.9	790	1	US-08-469-486-54	Sequence 54, Appl	494	337	24.5	812	1	US-08-248-629A-1	Sequence 1, Appli
422	342.5	24.9	790	2	US-08-469-486-54	Sequence 54, Appl	495	337	24.5	812	1	US-08-451-932-1	Sequence 1, Appli
423	342.5	24.9	791	2	US-09-131-995-1	Sequence 1, Appli	496	337	24.5	812	1	US-08-452-260-1	Sequence 1, Appli
424	342.5	24.9	791	2	US-08-832-087B-1	Sequence 1, Appli	497	337	24.5	812	1	US-08-326-785-1	Sequence 1, Appli
425	342.5	24.9	791	3	US-09-132-154-1	Sequence 1, Appli	498	337	24.5	812	2	US-08-612-788-1	Sequence 1, Appli
426	342.5	24.9	791	4	US-08-991-761A-6	Sequence 6, Appli	499	337	24.5	812	2	US-08-605-598B-1	Sequence 1, Appli
427	342.5	24.9	791	4	US-08-924-287A-1	Sequence 1, Appli	500	337	24.5	812	2	US-08-429-743-1	Sequence 1, Appli
428	342.5	24.9	810	1	US-07-854-603-2	Sequence 2, Appli	501	337	24.5	812	2	US-08-866-735-1	Sequence 1, Appli
429	342.5	24.9	810	1	US-08-147-000B-29	Sequence 29, Appl	502	337	24.5	812	2	US-09-066-028-1	Sequence 1, Appli
430	342.5	24.9	810	3	US-09-086-514-1	Sequence 5, Appli	503	337	24.5	812	4	US-09-335-325-1	Sequence 3, Appli
431	342.5	24.9	810	4	US-09-132-012-5	Sequence 1, Appli	504	337	24.5	812	4	US-09-335-325-1	Sequence 3, Appli
432	342.5	24.9	810	4	US-09-403-736-1	Sequence 1, Appli	505	337	24.5	812	4	US-08-991-761A-12	Sequence 12, Appl
433	342.5	24.9	810	4	US-09-701-265-1	Sequence 1, Appli	506	337	24.5	812	5	PCT-US95-05107-1	Sequence 1, Appli
434	342.5	24.9	810	6	5200340-8	Patent No. 5200340	507	336.5	24.5	435	3	US-09-008-271A-6	Sequence 6, Appli
435	342.5	24.9	810	6	5200340-8	Patent No. 5200340	508	336	24.5	415	1	US-08-073-531B-1	Sequence 1, Appli
436	342	24.9	234	1	US-08-684-862-3	Sequence 3, Appli	509	336	24.5	415	2	US-08-766-288-1	Sequence 1, Appli
437	342	24.9	273	2	US-09-016-366A-19	Sequence 19, Appl	510	336	24.5	790	4	US-08-991-761A-13	Sequence 13, Appl
438	342	24.9	273	2	US-08-978-404B-14	Sequence 14, Appl	511	334.5	24.3	446	4	US-10-177-661-4	Sequence 4, Appli
439	341.5	24.9	156	3	US-09-261-416-6	Sequence 6, Appli	512	334.5	24.3	477	4	US-10-177-661-4	Sequence 2, Appli
440	341.5	24.9	261	6	5270178-19	Patent No. 5270178	513	334.5	24.3	562	4	US-09-879-792-12	Sequence 12, Appl
441	341.5	24.9	261	6	5270178-20	Patent No. 5270178	514	334	24.3	316	4	US-09-387-375-9	Sequence 9, Appli
442	341.5	24.9	261	6	5270178-20	Patent No. 5270178	515	334	24.3	316	4	US-10-041-400A-9	Sequence 9, Appli
443	341.5	24.9	261	6	5270178-21	Patent No. 5270178	516	334	24.3	316	4	US-10-042-091A-9	Sequence 9, Appli
444	341	24.8	261	6	5270178-21	Patent No. 5270178	517	333.5	24.3	290	4	US-09-386-653A-7	Sequence 7, Appli
445	341	24.8	261	6	5270178-21	Patent No. 5270178	518	333.5	24.3	302	3	US-09-220-731-26	Sequence 26, Appl
446	341	24.8	306	4	US-09-386-642-53	Sequence 53, Appl	519	333.5	24.3	302	4	US-09-242-999-22	Sequence 22, Appl
447	341	24.8	415	4	US-08-118-748-2	Sequence 2, Appli	520	333	24.2	415	1	US-08-295-411-2	Sequence 2, Appli
448	340.5	24.8	230	1	US-08-456-840-47	Sequence 47, Appl	521	333	24.2	415	2	US-08-955-471-2	Sequence 2, Appli
449	340.5	24.8	230	1	US-08-266-407A-47	Sequence 47, Appl	522	333	24.2	415	5	PCT-US92-10242-2	Sequence 2, Appli
450	340.5	24.8	230	2	US-08-892-544-47	Sequence 47, Appl	523	332.5	24.2	638	2	US-08-681-151-3	Sequence 3, Appli
451	340.5	24.8	230	2	US-08-766-982-12	Sequence 12, Appl	524	332.5	24.2	810	4	US-08-991-761A-11	Sequence 11, Appl
452	340.5	24.8	230	3	US-08-944-483-53	Sequence 53, Appl	525	331	24.1	235	3	US-08-338-368-2	Sequence 2, Appli
453	340.5	24.8	230	3	US-09-296-219-12	Sequence 12, Appl	526	331	24.1	235	1	US-08-295-411-4	Sequence 4, Appli
454	340.5	24.8	244	4	US-09-601-318-4	Sequence 4, Appli	527	331	24.1	579	2	US-08-955-471-4	Sequence 4, Appli
455	340.5	24.8	244	4	US-09-601-318-5	Sequence 5, Appli	528	331	24.1	579	2	US-09-117-708-14	Sequence 14, Appl
456	340.5	24.8	244	4	US-09-601-318-6	Sequence 6, Appli	529	331	24.1	579	5	PCT-US92-10242-4	Sequence 4, Appli
457	340.5	24.8	244	4	US-09-601-318-7	Sequence 7, Appli	530	331	24.1	615	1	US-07-998-972A-3	Sequence 3, Appli
458	340.5	24.8	245	3	US-09-079-970A-6	Sequence 6, Appli	531	331	24.1	615	1	US-08-463-953-3	Sequence 3, Appli
459	340.5	24.8	245	3	US-09-601-318-1	Sequence 1, Appli	532	331	24.1	615	5	US-08-462-261-3	Sequence 3, Appli
460	340.5	24.8	267	2	US-09-016-366A-23	Sequence 23, Appl	533	331	24.1	615	5	PCT-US92-11357-3	Sequence 3, Appli
461	340.5	24.8	267	2	US-08-978-404B-18	Sequence 18, Appl	534	331	24.1	622	3	US-08-952-967-8	Sequence 8, Appli
462	340.5	24.8	267	2	US-09-917-254-101	Sequence 101, App	535	331	24.1	622	4	US-09-054-272-42	Sequence 42, Appl
463	340.5	24.8	300	3	US-08-705-875A-6	Sequence 6, Appli	536	330.5	24.1	560	4	US-09-949-016-6458	Sequence 6458, Ap
464	340.5	24.8	300	4	US-09-242-999-6	Sequence 6, Appli	537	330.5	24.1	560	4	US-09-912-559-3	Sequence 3, Appli
465	340	24.7	419	4	US-10-182-263-3	Sequence 3, Appli	538	330	24.0	221	3	US-08-944-483-54	Sequence 54, Appl



539	330	24.0	222	1	US-08-456-840-46	Sequence 46, Appl	612	321	23.4	300	1	US-08-448-937A-1	Sequence 1, Appl
540	330	24.0	222	1	US-08-266-407A-46	Sequence 46, Appl	613	321	23.4	315	4	US-09-386-653A-9	Sequence 9, Appl
541	330	24.0	222	2	US-08-892-544-46	Sequence 46, Appl	614	321	23.4	655	1	US-08-148-910-12	Sequence 12, Appl
542	330	24.0	222	6	5223425-6	Patent No. 5223425	615	321	23.4	655	1	US-08-448-937A-12	Sequence 9, Appl
543	330	24.0	222	6	5223425-6	Patent No. 5223425	616	321	23.4	809	4	US-08-991-761A-9	Sequence 11, Appl
544	329.5	24.0	230	4	US-09-601-318-3	Sequence 3, Appl	617	319.5	23.3	240	1	US-08-278-091-11	Sequence 11, Appl
545	329.5	24.0	376	2	US-08-558-269-10	Sequence 10, Appl	618	319.5	23.3	240	1	US-08-483-859-11	Sequence 11, Appl
546	329.5	24.0	376	3	US-09-410-882-10	Sequence 10, Appl	619	319.5	23.3	240	1	US-08-472-173-11	Sequence 11, Appl
547	329	23.9	259	3	US-08-944-483-52	Sequence 52, Appl	620	319.5	23.3	240	2	US-08-487-167-11	Sequence 11, Appl
548	328.5	23.9	338	3	US-08-944-483-64	Sequence 64, Appl	621	319.5	23.3	240	2	US-08-482-816-11	Sequence 11, Appl
549	328.5	23.9	338	4	US-08-991-761A-10	Sequence 10, Appl	622	319.5	23.3	240	2	US-08-296-149-11	Sequence 11, Appl
550	327.5	23.8	151	3	US-09-518-046-21	Sequence 21, Appl	623	319.5	23.3	240	2	US-08-801-499-11	Sequence 11, Appl
551	327.5	23.8	154	3	US-09-261-416-7	Sequence 7, Appl	624	319.5	23.3	240	2	US-08-615-271-11	Sequence 11, Appl
552	327	23.8	241	3	US-08-944-483-60	Sequence 60, Appl	625	319.5	23.3	240	3	US-09-074-660-11	Sequence 11, Appl
553	327	23.8	255	1	US-08-650-129-5	Sequence 5, Appl	626	319.5	23.3	240	3	US-09-074-659-11	Sequence 11, Appl
554	327	23.8	255	3	US-08-984-417-5	Sequence 5, Appl	627	319.5	23.3	240	3	US-09-106-468-11	Sequence 11, Appl
555	326.5	23.7	144	4	US-09-618-259-1	Sequence 1, Appl	628	319.5	23.3	240	3	US-09-106-466A-11	Sequence 11, Appl
556	325.5	23.7	261	3	US-08-163-919A-2	Sequence 2, Appl	629	319.5	23.3	240	3	US-09-106-467-11	Sequence 11, Appl
557	325.5	23.7	261	4	US-08-462-515-2	Sequence 2, Appl	630	319.5	23.3	254	3	US-08-944-483-50	Sequence 50, Appl
558	325.5	23.7	261	5	PCT-US94-14073-2	Sequence 2, Appl	631	318	23.1	295	4	US-10-165-442-3	Sequence 3, Appl
559	325	23.7	226	1	US-08-650-129-4	Sequence 4, Appl	632	317.5	23.1	245	3	US-08-944-483-69	Sequence 69, Appl
560	325	23.7	226	3	US-08-984-417-4	Sequence 4, Appl	633	317	23.1	232	4	US-10-165-442-1	Sequence 45, Appl
561	324.5	23.6	228	1	US-08-278-091-10	Sequence 10, Appl	634	317	23.1	295	4	US-10-165-442-2	Sequence 1, Appl
562	324.5	23.6	228	1	US-08-483-859-10	Sequence 10, Appl	635	316.5	23.0	226	1	US-07-929-198-2	Sequence 2, Appl
563	324.5	23.6	228	1	US-08-472-173-10	Sequence 10, Appl	636	316.5	23.0	226	1	US-07-929-198-6	Sequence 6, Appl
564	324.5	23.6	228	2	US-08-487-167-10	Sequence 10, Appl	637	316.5	23.0	226	2	US-08-557-146-15	Sequence 15, Appl
565	324.5	23.6	228	2	US-08-482-816-10	Sequence 10, Appl	638	316.5	23.0	226	2	US-09-154-344-15	Sequence 15, Appl
566	324.5	23.6	228	2	US-08-296-149-10	Sequence 10, Appl	639	316.5	23.0	226	3	US-08-944-483-43	Sequence 43, Appl
567	324.5	23.6	228	2	US-08-801-499-10	Sequence 10, Appl	640	316	23.0	246	3	US-08-906-769-127	Sequence 127, App
568	324.5	23.6	228	2	US-08-615-271-10	Sequence 10, Appl	641	316	23.0	246	3	US-08-906-616-127	Sequence 127, App
569	324.5	23.6	228	3	US-09-074-660-10	Sequence 10, Appl	642	316	23.0	246	3	US-08-639-075A-127	Sequence 127, App
570	324.5	23.6	228	3	US-09-074-659-10	Sequence 10, Appl	643	316	23.0	246	3	US-09-012-431-127	Sequence 127, App
571	324.5	23.6	228	3	US-09-106-468-10	Sequence 10, Appl	644	316	23.0	246	3	US-09-012-692-127	Sequence 127, App
572	324.5	23.6	228	3	US-09-106-468A-10	Sequence 10, Appl	645	316	23.0	246	3	US-08-906-613-127	Sequence 127, App
573	324.5	23.6	228	3	US-09-106-467-10	Sequence 10, Appl	646	316	23.0	259	4	US-10-165-442-4	Sequence 4, Appl
574	323.5	23.5	275	2	US-09-016-366A-17	Sequence 17, Appl	647	315.5	23.0	254	3	US-09-578-303-5	Sequence 5, Appl
575	323.5	23.5	275	2	US-08-978-404B-12	Sequence 12, Appl	648	315.5	23.0	292	4	US-09-607-745-9	Sequence 9, Appl
576	323.5	23.5	406	1	US-08-293-778-24	Sequence 24, Appl	649	315.5	23.0	300	3	US-08-705-875A-4	Sequence 4, Appl
577	323.5	23.5	406	1	US-08-295-411-5	Sequence 5, Appl	650	315.5	23.0	300	3	US-09-230-731-21	Sequence 21, Appl
578	323.5	23.5	406	2	US-08-955-471-5	Sequence 5, Appl	651	315.5	23.0	300	4	US-03-242-999-4	Sequence 4, Appl
579	323.5	23.5	406	4	US-08-782-587B-1	Sequence 1, Appl	652	315.5	23.0	487	1	US-08-469-486-53	Sequence 53, Appl
580	323.5	23.5	406	4	US-09-782-587B-3	Sequence 3, Appl	653	315.5	23.0	487	2	US-08-469-658-53	Sequence 53, Appl
581	323.5	23.5	406	5	PCT-US92-10242-5	Sequence 5, Appl	654	315.5	23.0	492	1	US-08-469-486-2	Sequence 2, Appl
582	323.5	23.5	444	1	US-08-475-845-2	Sequence 2, Appl	655	315.5	23.0	492	2	US-08-469-658-2	Sequence 2, Appl
583	323.5	23.5	444	2	US-08-327-690-2	Sequence 2, Appl	656	315	22.9	259	4	US-10-165-442-2	Sequence 2, Appl
584	323.5	23.5	444	2	US-08-660-289-2	Sequence 2, Appl	657	315	22.9	691	4	US-09-949-016-7775	Sequence 7775, Ap
585	323.5	23.5	444	2	US-08-537-807-2	Sequence 2, Appl	658	314.5	22.9	283	4	US-03-244-111-2	Sequence 2, Appl
586	323.5	23.5	444	2	US-08-871-003-2	Sequence 2, Appl	659	314	22.9	855	2	US-09-027-337-2	Sequence 2, Appl
587	323.5	23.5	444	2	US-08-464-233-2	Sequence 2, Appl	660	314	22.9	855	4	US-09-644-600-2	Sequence 2, Appl
588	323.5	23.5	444	3	US-09-189-607-2	Sequence 2, Appl	661	314	22.9	855	4	US-09-654-600A-2	Sequence 2, Appl
589	323.5	23.5	444	3	US-09-378-907-2	Sequence 2, Appl	662	313.5	22.8	226	1	US-07-929-198-4	Sequence 4, Appl
590	323.5	23.5	444	5	PCT-US94-05779-2	Sequence 2, Appl	663	312.5	22.7	242	3	US-09-959-392-34	Sequence 34, Appl
591	323.5	23.5	461	4	US-09-949-016-8839	Sequence 8839, Ap	664	312	22.7	248	3	US-08-944-483-71	Sequence 71, Appl
592	323.5	23.5	466	1	US-07-882-202A-4	Sequence 4, Appl	665	311.5	22.7	251	3	US-08-944-483-47	Sequence 47, Appl
593	323.5	23.5	466	1	US-08-021-615A-4	Sequence 4, Appl	666	311	22.6	383	2	US-08-558-269-6	Sequence 6, Appl
594	323.5	23.5	466	1	US-08-321-777-4	Sequence 4, Appl	667	311	22.6	383	3	US-09-410-882-6	Sequence 6, Appl
595	323.5	23.5	466	3	US-09-009-217-14	Sequence 14, Appl	668	311	22.6	798	1	US-08-200-900A-2	Sequence 2, Appl
596	323.5	23.5	466	3	US-09-009-656-14	Sequence 4, Appl	669	311	22.6	798	4	US-08-794-042-2	Sequence 2, Appl
597	323.5	23.5	466	5	PCT-US93-04493-4	Sequence 4, Appl	670	311	22.6	798	5	PCT-US94-00616-2	Sequence 2, Appl
598	323.5	23.5	483	4	US-09-949-016-9523	Sequence 9523, Ap	671	311	22.6	812	4	US-09-192-012-9	Sequence 9, Appl
599	322.5	23.5	285	4	US-09-023-942A-26	Sequence 26, Appl	672	311	22.6	1042	4	US-09-959-392-2	Sequence 2, Appl
600	322.5	23.5	560	4	US-09-912-559-4	Sequence 4, Appl	673	310.5	22.6	247	2	US-08-978-404B-47	Sequence 47, Appl
601	322	23.4	207	4	US-10-000-489-54	Sequence 54, Appl	674	309.5	22.5	241	4	US-09-657-986B-2	Sequence 2, Appl
602	322	23.4	699	4	US-09-949-016-6138	Sequence 6138, Ap	675	309.5	22.5	492	4	US-03-685-166A-895	Sequence 895, App
603	322	23.4	717	4	US-09-949-016-11182	Sequence 11182, A	676	309.5	22.5	492	4	US-08-879-792-14	Sequence 14, Appl
604	321.5	23.4	255	2	US-09-027-337-7	Sequence 7, Appl	677	309.5	22.5	492	4	US-09-679-426-895	Sequence 895, App
605	321.5	23.4	255	4	US-09-644-600-7	Sequence 7, Appl	678	309.5	22.5	492	4	US-09-759-143-895	Sequence 895, App
606	321.5	23.4	255	4	US-09-654-600A-7	Sequence 7, Appl	679	308.5	22.5	243	3	US-08-944-483-70	Sequence 70, Appl
607	321.5	23.4	418	4	US-10-177-661-6	Sequence 6, Appl	680	308.5	22.5	319	4	US-09-270-767-42672	Sequence 42672, A
608	321	23.4	248	2	US-08-851-974-3	Sequence 3, Appl	681	308	22.4	232	4	US-09-959-392-32	Sequence 32, Appl
609	321	23.4	248	2	US-09-213-390-3	Sequence 3, Appl	682	308	22.4	317	4	US-09-386-629-7	Sequence 7, Appl
610	321	23.4	269	2	US-08-978-404B-10	Sequence 10, Appl	683	308	22.4	317	4	US-09-907-795A-263	Sequence 263, App
611	321	23.4	300	1	US-08-148-910-1	Sequence 1, Appl	684	308	22.4	317	4	US-09-905-125A-263	Sequence 263, App

685	308	22.4	317	4	US-09-902-775A-263	Sequence 263, App	758	304	22.1	562	6	5185259-3	Patent No. 5185259
686	308	22.4	317	4	US-09-906-700-263	Sequence 263, App	759	304	22.1	562	6	5200340-2	Patent No. 5200340
687	308	22.4	317	4	US-09-903-603A-263	Sequence 263, App	760	304	22.1	562	6	5244676-5	Patent No. 5244676
688	308	22.4	317	4	US-09-904-920A-263	Sequence 263, App	761	304	22.1	562	6	5344773-2	Patent No. 5344773
689	308	22.4	317	4	US-09-909-624A-263	Sequence 263, App	762	304	22.1	562	6	5185259-3	Patent No. 5185259
690	308	22.4	317	4	US-09-905-381A-263	Sequence 263, App	763	304	22.1	562	6	5200340-2	Patent No. 5200340
691	308	22.4	317	4	US-09-906-618-263	Sequence 263, App	764	304	22.1	562	6	5244676-5	Patent No. 5244676
692	308	22.4	356	2	US-08-681-151-1	Sequence 1, Appli	765	304	22.1	562	6	5344773-2	Patent No. 5344773
693	307.5	22.4	376	4	US-08-820-002-2	Sequence 2, Appli	766	304	22.1	587	4	US-09-949-016-11501	Sequence 11501, A
694	307	22.3	268	1	US-08-568-031-2	Sequence 2, Appli	767	303.5	22.1	234	4	US-09-513-999C-7815	Sequence 7815, Ap
695	307	22.3	268	1	US-08-966-319-2	Sequence 2, Appli	768	303.5	22.1	278	4	US-08-392-828C-4	Sequence 4, Appli
696	307	22.3	268	3	US-09-153-304-2	Sequence 2, Appli	769	303.5	22.1	278	3	US-09-330-945-4	Sequence 4, Appli
697	307	22.3	355	2	US-08-811-949-47	Sequence 47, Appli	770	303	22.1	258	4	US-09-949-016-10661	Sequence 10661, A
698	307	22.3	355	2	US-08-811-949-59	Sequence 59, Appli	771	303	22.1	355	2	US-08-811-949-53	Sequence 53, Appli
699	307	22.3	417	4	US-08-820-002-4	Sequence 4, Appli	772	303	22.1	389	2	US-08-811-949-67	Sequence 67, Appli
700	307	22.3	437	2	US-08-811-949-51	Sequence 51, Appli	773	303	22.1	437	2	US-08-811-949-55	Sequence 55, Appli
701	307	22.3	452	4	US-09-949-016-7182	Sequence 7182, Ap	774	303	22.1	527	4	US-09-600-985-1	Sequence 1, Appli
702	307	22.3	527	2	US-08-811-949-39	Sequence 39, Appli	775	302.5	22.0	1113	4	US-09-959-392-4	Sequence 4, Appli
703	306	22.3	256	2	US-09-027-337-3	Sequence 3, Appli	776	302	22.0	389	2	US-08-811-949-65	Sequence 65, Appli
704	306	22.3	256	4	US-09-644-600-3	Sequence 3, Appli	777	302	22.0	477	2	US-08-560-098A-51	Sequence 51, Appli
705	306	22.3	256	4	US-09-654-600A-3	Sequence 3, Appli	778	302	22.0	527	4	US-09-600-985-2	Sequence 2, Appli
706	306	22.3	437	2	US-08-811-949-57	Sequence 57, Appli	779	302	22.0	527	4	US-09-600-985-3	Sequence 3, Appli
707	305.5	22.2	146	4	US-09-618-259-3	Sequence 3, Appli	780	301.5	21.9	226	3	US-08-944-483-41	Sequence 41, Appli
708	305	22.2	247	2	US-08-851-974-1	Sequence 1, Appli	781	301	21.9	255	1	US-08-208-007A-14	Sequence 14, Appli
709	305	22.2	247	2	US-08-851-974-4	Sequence 4, Appli	782	301	21.9	255	3	US-08-915-095A-14	Sequence 14, Appli
710	305	22.2	247	2	US-09-213-390-1	Sequence 1, Appli	783	301	21.9	255	3	US-08-798-096-14	Sequence 14, Appli
711	305	22.2	247	2	US-09-213-390-4	Sequence 4, Appli	784	301	21.9	255	4	US-08-798-095A-14	Sequence 14, Appli
712	305	22.2	247	4	US-09-949-016-6457	Sequence 6457, Ap	785	301	21.9	255	4	US-09-953-956-14	Sequence 14, Appli
713	305	22.2	437	2	US-08-811-949-16	Sequence 16, Appli	786	301	21.9	255	4	US-08-553-125A-14	Sequence 14, Appli
714	304.5	22.2	258	3	US-09-004-731-19	Sequence 19, Appli	787	301	21.9	255	4	US-10-114-464-14	Sequence 14, Appli
715	304.5	22.2	258	3	US-09-004-731-19	Sequence 19, Appli	788	301	21.9	257	4	US-09-949-016-10662	Sequence 10662, A
716	304.5	22.2	258	3	US-08-749-699-16	Sequence 16, Appli	789	301	21.9	527	6	5520913-1	Patent No. 5520913
717	304.5	22.2	258	3	US-08-749-699-19	Sequence 19, Appli	790	301	21.9	527	6	5520913-1	Patent No. 5520913
718	304.5	22.2	258	4	US-09-004-729-16	Sequence 16, Appli	791	300	21.8	233	4	US-09-636-382A-24	Sequence 24, Appli
719	304.5	22.2	258	4	US-09-004-729-19	Sequence 19, Appli	792	298	21.7	347	2	US-08-811-949-1	Sequence 1, Appli
720	304.5	22.2	314	4	US-09-636-382A-2	Sequence 2, Appli	793	297	21.6	237	3	US-08-163-919A-3	Sequence 3, Appli
721	304.5	22.2	384	3	US-09-032-215-22	Sequence 22, Appli	794	297	21.6	237	4	US-08-462-515-3	Sequence 3, Appli
722	304.5	22.2	393	4	US-09-759-143-934	Sequence 934, App	795	297	21.6	237	5	PCT-US94-14073-3	Sequence 3, Appli
723	304.5	22.2	492	3	US-09-342-749-2	Sequence 2, Appli	796	297	21.6	252	2	US-08-944-483-72	Sequence 72, Appli
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725	304.5	22.2	492	4	US-09-759-143-932	Sequence 932, App	798	297	21.6	253	4	US-09-644-600-8	Sequence 8, Appli
726	304.5	22.2	510	4	US-09-949-016-11074	Sequence 11074, A	799	297	21.6	253	4	US-09-654-600A-8	Sequence 8, Appli
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729	304	22.1	255	3	US-08-944-483-67	Sequence 67, Appli	802	297	21.6	354	2	US-08-811-949-61	Sequence 61, Appli
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731	304	22.1	327	4	US-09-386-629-8	Sequence 8, Appli	804	297	21.6	521	4	US-09-949-016-11081	Sequence 11081, A
732	304	22.1	355	1	US-08-137-116-1	Sequence 1, Appli	805	297	21.6	521	4	US-09-949-016-11082	Sequence 11082, A
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735	304	22.1	355	1	US-08-427-640-6	Sequence 6, Appli	808	296.5	21.6	224	1	US-08-483-859-12	Sequence 12, Appli
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737	304	22.1	355	1	US-08-217-616-1	Sequence 1, Appli	810	296.5	21.6	224	2	US-08-487-167-12	Sequence 12, Appli
738	304	22.1	355	2	US-08-811-949-45	Sequence 45, Appli	811	296.5	21.6	224	2	US-08-482-816-12	Sequence 12, Appli
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741	304	22.1	355	6	5232356-1	Patent No. 5232356	814	296.5	21.6	224	2	US-08-615-271-12	Sequence 12, Appli
742	304	22.1	356	1	US-08-427-640-4	Sequence 4, Appli	815	296.5	21.6	224	2	US-09-074-660-12	Sequence 12, Appli
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744	304	22.1	378	3	US-09-553-498-10	Sequence 10, Appli	817	296.5	21.6	224	3	US-09-106-468-12	Sequence 12, Appli
745	304	22.1	378	4	US-09-618-869-10	Sequence 10, Appli	818	296.5	21.6	224	3	US-09-106-466A-12	Sequence 12, Appli
746	304	22.1	433	4	US-09-949-016-8220	Sequence 8220, Ap	819	296.5	21.6	224	3	US-09-106-467-12	Sequence 12, Appli
747	304	22.1	472	2	US-08-811-949-63	Sequence 63, Appli	820	296.5	21.6	246	4	US-09-205-258-1149	Sequence 1149, Ap
748	304	22.1	527	1	US-07-609-510B-16	Sequence 16, Appli	821	296.5	21.6	254	2	US-08-560-098A-49	Sequence 49, Appli
749	304	22.1	527	4	US-09-612-314A-51	Sequence 51, Appli	822	296.5	21.6	254	4	US-08-880-503-5	Sequence 5, Appli
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751	304	22.1	527	6	5185259-8	Patent No. 5185259	824	296.5	21.6	331	2	US-08-560-098A-46	Sequence 46, Appli
752	304	22.1	527	6	5185259-8	Patent No. 5185259	825	296.5	21.6	365	1	US-08-093-741-83	Sequence 83, Appli
753	304	22.1	562	2	US-08-811-949-43	Sequence 43, Appli	826	296.5	21.6	365	1	US-08-720-012-83	Sequence 83, Appli
754	304	22.1	562	2	US-08-560-098A-50	Sequence 50, Appli	827	296.5	21.6	393	2	US-08-560-098A-44	Sequence 44, Appli
755	304	22.1	562	2	US-08-883-795A-38	Sequence 38, Appli	828	296.5	21.6	393	3	US-08-967-024C-24	Sequence 24, Appli
756	304	22.1	562	4	US-09-703-695A-4	Sequence 4, Appli	829	296.5	21.6	393	3	US-08-967-024C-25	Sequence 25, Appli
757	304	22.1	562	4	US-10-443-701-4	Sequence 4, Appli	830	296.5	21.6	403	4	US-09-880-503-6	Sequence 6, Appli

831	236.5	21.6	411	1	US-08-087-163-1	Sequence 1, Appli	904	282	20.5	244	3	US-08-944-483-74	Sequence 74, Appl
832	236.5	21.6	411	1	US-08-286-748B-18	Sequence 18, Appl	905	279	20.3	902	4	US-09-644-600-10	Sequence 10, Appl
833	236.5	21.6	411	1	US-08-153-799-18	Sequence 18, Appl	906	279	20.3	902	4	US-09-654-600A-10	Sequence 10, Appl
834	236.5	21.6	411	2	US-08-560-098A-48	Sequence 48, Appl	907	277.5	20.2	242	3	US-08-944-483-58	Sequence 58, Appl
835	236.5	21.6	411	2	US-08-880-503-3	Sequence 3, Appli	908	277	20.2	488	4	US-09-367-777-44	Sequence 44, Appl
836	236.5	21.6	430	6	5219569-2	Patent No. 5219569	909	277	20.2	488	4	US-09-367-791A-27	Sequence 27, Appl
837	236.5	21.6	430	6	5219569-2	Patent No. 5219569	910	276	20.1	306	1	US-08-330-978-1	Sequence 1, Appli
838	236.5	21.6	431	4	US-09-101-272G-1	Sequence 1, Appli	911	276	20.1	306	1	US-08-474-042-1	Sequence 1, Appli
839	236.5	21.6	431	6	5188829-1	Patent No. 5188829	912	276	20.1	306	1	US-08-484-558-1	Sequence 1, Appli
840	236.5	21.6	431	6	5188829-1	Patent No. 5188829	913	276	20.1	306	1	US-08-774-592-1	Sequence 1, Appli
841	236.5	21.6	432	2	US-08-560-098A-47	Sequence 47, Appl	914	276	20.1	437	1	US-08-487-037-2	Sequence 2, Appli
842	236.5	21.6	269	4	US-08-715-994-2	Sequence 2, Appli	915	276	20.1	448	2	US-08-295-411-3	Sequence 3, Appli
843	236.5	21.6	283	3	US-08-807-151-1	Sequence 1, Appli	916	276	20.1	448	2	US-08-955-471-3	Sequence 3, Appli
844	236.5	21.6	283	3	US-09-478-957-1	Sequence 1, Appli	917	276	20.1	448	5	PCT-US92-10268-1	Sequence 1, Appli
845	236.5	21.6	454	3	US-09-518-046-2	Sequence 2, Appli	918	276	20.1	448	5	PCT-US92-10242-3	Sequence 3, Appli
846	236.5	21.6	294	4	US-09-032-215-32	Sequence 32, Appl	919	276	20.1	488	1	US-08-487-037-1	Sequence 1, Appli
847	236.5	21.6	239	3	US-08-944-483-61	Sequence 61, Appl	920	276	20.1	496	4	US-09-949-016-9524	Sequence 9524, Ap
848	236.5	21.6	411	4	US-09-403-736-2	Sequence 2, Appli	921	274.5	20.0	211	3	US-09-220-731-25	Sequence 25, Appl
849	236.5	21.6	430	1	US-07-942-157A-3	Sequence 3, Appli	922	274.5	20.0	211	4	US-09-242-999-20	Sequence 20, Appl
850	236.5	21.6	237	3	US-09-004-731-22	Sequence 22, Appl	923	274	19.9	241	1	US-08-330-978-4	Sequence 4, Appli
851	236.5	21.6	237	3	US-08-749-699-22	Sequence 22, Appl	924	274	19.9	241	1	US-08-474-042-4	Sequence 4, Appli
852	236.5	21.6	237	4	US-09-004-729-22	Sequence 22, Appl	925	274	19.9	241	1	US-08-484-558-4	Sequence 4, Appli
853	236.5	21.6	256	3	US-08-906-769-89	Sequence 89, Appl	926	274	19.9	241	1	US-08-774-592-4	Sequence 4, Appli
854	236.5	21.6	256	3	US-08-906-616-89	Sequence 89, Appl	927	274	19.9	254	1	US-08-330-978-3	Sequence 3, Appli
855	236.5	21.6	256	3	US-08-817-795-89	Sequence 89, Appl	928	274	19.9	254	1	US-08-474-042-3	Sequence 3, Appli
856	236.5	21.6	256	3	US-08-639-075A-89	Sequence 89, Appl	929	274	19.9	254	1	US-08-484-558-3	Sequence 3, Appli
857	236.5	21.6	256	3	US-09-012-431-89	Sequence 89, Appl	930	274	19.9	254	1	US-08-774-592-3	Sequence 3, Appli
858	236.5	21.6	256	3	US-09-012-692-89	Sequence 89, Appl	931	272	19.8	253	3	US-08-906-769-131	Sequence 131, App
859	236.5	21.6	256	3	US-08-906-613-89	Sequence 89, Appl	932	272	19.8	253	3	US-08-906-616-131	Sequence 131, App
860	236.5	21.6	256	5	PCT-US95-14442A-89	Sequence 89, Appl	933	272	19.8	253	3	US-08-639-075A-131	Sequence 131, App
861	236.5	21.6	414	4	US-09-270-767-46426	Sequence 46426, A	934	272	19.8	253	3	US-09-012-431-131	Sequence 131, App
862	236.5	21.6	242	3	US-08-944-483-57	Sequence 57, Appl	935	272	19.8	253	3	US-09-012-692-131	Sequence 131, App
863	236.5	21.6	253	3	US-08-944-483-73	Sequence 73, Appl	936	272	19.8	253	3	US-08-906-613-131	Sequence 131, App
864	236.5	21.6	416	2	US-09-000-846-2	Sequence 2, Appli	937	270	19.7	251	3	US-08-944-483-28	Sequence 28, Appl
865	236.5	21.6	235	2	US-08-557-146-14	Sequence 14, Appl	938	269	19.6	256	4	US-08-355-456C-23	Sequence 23, Appl
866	236.5	21.6	235	2	US-08-154-344-14	Sequence 14, Appl	939	269	19.6	256	4	US-08-487-042B-23	Sequence 23, Appl
867	236.5	21.6	235	3	US-08-807-151-3	Sequence 3, Appli	940	268	19.5	256	2	US-08-230-428B-4	Sequence 4, Appli
868	236.5	21.6	235	3	US-08-944-483-42	Sequence 42, Appl	941	268	19.5	437	1	US-08-487-037-3	Sequence 3, Appli
869	236.5	21.6	235	3	US-09-478-957-3	Sequence 3, Appli	942	267.5	19.5	266	3	US-09-004-731-24	Sequence 24, Appl
870	236.5	21.6	223	1	US-07-956-848A-41	Sequence 41, Appl	943	267.5	19.5	266	3	US-08-749-699-24	Sequence 24, Appl
871	236.5	21.6	223	1	US-08-471-956-41	Sequence 41, Appl	944	267.5	19.5	266	3	US-09-004-729-24	Sequence 24, Appl
872	236.5	21.6	583	4	US-09-976-594-837	Sequence 837, App	945	265.5	19.3	197	1	US-08-456-840-48	Sequence 48, Appl
873	236.5	21.6	255	3	US-08-906-769-91	Sequence 91, Appl	946	265.5	19.3	197	2	US-08-266-407A-48	Sequence 48, Appl
874	236.5	21.6	255	3	US-08-906-616-91	Sequence 91, Appl	947	265.5	19.3	197	2	US-08-892-544-48	Sequence 48, Appl
875	236.5	21.6	255	3	US-08-817-795-91	Sequence 91, Appl	948	264.5	19.3	248	2	US-08-238-130-2	Sequence 2, Appli
876	236.5	21.6	255	3	US-08-639-075A-91	Sequence 91, Appl	949	264.5	19.3	248	2	US-08-921-426-4	Sequence 4, Appli
877	236.5	21.6	255	3	US-09-012-431-91	Sequence 91, Appl	950	264.5	19.3	248	3	US-08-816-915-4	Sequence 4, Appli
878	236.5	21.6	255	3	US-08-012-692-91	Sequence 91, Appl	951	264.5	19.3	248	5	PCT-US95-07743-4	Sequence 2, Appli
879	236.5	21.6	255	3	US-08-906-613-91	Sequence 91, Appl	952	264.5	19.3	249	3	US-09-578-303-2	Sequence 2, Appli
880	236.5	21.6	255	5	PCT-US95-14442A-91	Sequence 91, Appl	953	264	19.2	250	3	US-08-944-483-68	Sequence 68, Appl
881	236.5	21.6	268	1	US-08-270-584A-2	Sequence 2, Appli	954	264	19.2	256	4	US-09-949-016-6271	Sequence 6271, Ap
882	236.5	21.6	268	2	US-08-765-192-2	Sequence 2, Appli	955	263.5	19.2	222	2	US-08-491-204A-18	Sequence 18, Appl
883	236.5	21.6	268	3	US-09-139-793-2	Sequence 2, Appli	956	263.5	19.2	221	4	US-09-949-016-6112	Sequence 6112, Ap
884	236.5	21.6	227	3	US-08-944-483-40	Sequence 40, Appl	957	263.5	19.2	255	4	US-09-949-016-9690	Sequence 9690, Ap
885	236.5	21.6	218	3	US-09-734-675-4	Sequence 4, Appli	958	263	19.1	252	3	US-08-906-769-103	Sequence 103, App
886	236.5	21.6	228	3	US-09-578-303-3	Sequence 3, Appli	959	263	19.1	252	3	US-08-906-616-103	Sequence 103, App
887	236.5	21.6	228	3	US-09-004-731-10	Sequence 10, Appl	960	263	19.1	252	3	US-08-817-795-103	Sequence 103, App
888	236.5	21.6	228	3	US-08-749-699-10	Sequence 10, Appl	961	263	19.1	252	3	US-08-639-075A-103	Sequence 103, App
889	236.5	21.6	228	4	US-09-004-729-10	Sequence 10, Appl	962	263	19.1	252	3	US-09-012-431-103	Sequence 103, App
890	236.5	21.6	228	4	US-09-205-258-1150	Sequence 1150, Ap	963	263	19.1	252	3	US-09-012-692-103	Sequence 103, App
891	236.5	21.6	225	3	US-09-004-731-13	Sequence 13, Appl	964	263	19.1	252	3	US-08-906-613-103	Sequence 103, App
892	236.5	21.6	225	3	US-08-749-699-13	Sequence 13, Appl	965	263	19.1	252	5	PCT-US95-14442A-103	Sequence 103, App
893	236.5	21.6	225	4	US-09-004-729-13	Sequence 13, Appl	966	262.5	19.1	233	3	US-09-004-731-27	Sequence 27, Appl
894	236.5	21.6	225	3	US-08-906-769-83	Sequence 83, Appl	967	262.5	19.1	233	4	US-08-749-699-27	Sequence 27, Appl
895	236.5	21.6	225	3	US-08-906-616-83	Sequence 83, Appl	968	262.5	19.1	233	4	US-09-004-729-27	Sequence 27, Appl
896	236.5	21.6	225	3	US-08-817-795-83	Sequence 83, Appl	969	261.5	19.0	222	1	US-07-969-931-9	Sequence 9, Appli
897	236.5	21.6	225	3	US-08-639-075A-83	Sequence 83, Appl	970	261.5	19.0	222	1	US-07-855-417A-9	Sequence 9, Appli
898	236.5	21.6	225	3	US-09-012-431-83	Sequence 83, Appl	971	261.5	19.0	225	3	US-08-944-483-32	Sequence 32, Appl
899	236.5	21.6	225	3	US-09-012-692-83	Sequence 83, Appl	972	257.5	18.7	224	1	US-08-553-516-2	Sequence 2, Appli
900	236.5	21.6	225	3	US-08-906-613-83	Sequence 83, Appl	973	256	18.6	267	3	US-08-906-769-145	Sequence 145, App
901	236.5	21.6	225	5	PCT-US95-14442A-83	Sequence 83, Appl	974	256	18.6	267	3	US-08-906-616-145	Sequence 145, App
902	236.5	21.6	268	3	US-09-032-215-42	Sequence 42, Appl	975	256	18.6	267	3	US-08-639-075A-145	Sequence 145, App
903	236.5	21.6	144	4	US-09-618-259-4	Sequence 4, Appli	976	256	18.6	267	3	US-09-004-731-67	Sequence 67, Appl

977	256	18.6	267	3	US-09-012-431-145	Sequence 145, App	1050	226	16.4	697	3	US-08-462-040-50	Sequence 50, Appl
978	256	18.6	267	3	US-08-749-699-67	Sequence 67, Appl	1051	226	16.4	723	1	US-07-838-410-1	Sequence 1, Appl
979	256	18.6	267	3	US-09-012-692-145	Sequence 145, App	1052	226	16.4	723	1	US-08-290-937B-1	Sequence 2, Appl
980	256	18.6	267	3	US-08-906-613-145	Sequence 145, App	1053	226	16.4	723	1	US-08-290-937B-2	Sequence 3, Appl
981	256	18.6	267	4	US-09-004-729-67	Sequence 2, Appl	1054	226	16.4	723	1	US-08-404-643-1	Sequence 1, Appl
982	256	18.6	405	3	US-09-734-675-2	Sequence 2, Appl	1055	226	16.4	723	1	US-08-194-326-1	Sequence 1, Appl
983	254	18.5	242	3	US-09-004-731-41	Sequence 41, Appl	1056	226	16.4	723	3	US-09-194-326-2	Sequence 2, Appl
984	254	18.5	242	3	US-08-749-699-41	Sequence 41, Appl	1057	226	16.4	723	3	US-09-194-326-3	Sequence 3, Appl
985	254	18.5	242	4	US-09-004-729-41	Sequence 41, Appl	1058	226	16.4	723	3	US-08-700-519J-19	Sequence 19, Appl
986	254	18.5	255	4	US-09-270-767-44361	Sequence 44361, A	1059	226	16.4	723	4	US-09-600-991-18	Sequence 18, Appl
987	253	18.4	182	4	US-09-328-925-12	Sequence 12, Appl	1060	226	16.4	723	4	US-08-605-221-4	Sequence 4, Appl
988	253	18.4	231	4	US-08-395-456C-25	Sequence 25, Appl	1061	226	16.4	723	4	US-08-605-221-4	Sequence 10, Appl
989	253	18.4	242	3	US-09-032-215-47	Sequence 17, Appl	1062	226	16.4	723	4	US-09-601-040A-10	Sequence 2, Appl
990	252.5	18.4	221	2	US-08-925-708-1	Sequence 1, Appl	1063	226	16.4	728	1	US-07-815-333A-2	Sequence 2, Appl
991	252.5	18.4	239	3	US-09-004-731-44	Sequence 44, Appl	1064	226	16.4	728	1	US-08-087-783A-22	Sequence 22, Appl
992	252.5	18.4	239	3	US-08-749-699-44	Sequence 44, Appl	1065	226	16.4	728	4	US-08-087-783A-22	Sequence 2, Appl
993	252.5	18.4	239	4	US-09-004-729-44	Sequence 44, Appl	1066	222	16.2	723	3	US-08-030-410-3	Sequence 3, Appl
994	252.5	18.4	247	3	US-08-944-483-49	Sequence 49, Appl	1067	222	16.2	213	3	US-08-906-769-149	Sequence 149, App
995	252	18.3	229	4	US-08-395-456C-27	Sequence 27, Appl	1068	222	16.2	213	3	US-08-906-616-149	Sequence 149, App
996	251	18.3	229	2	US-08-394-600B-20	Sequence 20, Appl	1069	222	16.2	213	3	US-08-639-075A-149	Sequence 149, App
997	251	18.3	229	4	US-08-395-456C-20	Sequence 20, Appl	1070	222	16.2	213	3	US-09-012-431-149	Sequence 149, App
998	251	18.3	229	4	US-08-487-453A-20	Sequence 20, Appl	1071	222	16.2	213	3	US-09-012-692-149	Sequence 149, App
999	251	18.3	229	5	PCT-US95-025113-20	Sequence 20, Appl	1072	222	16.2	213	3	US-08-906-613-149	Sequence 149, App
1000	250	18.2	352	4	US-09-902-540-9796	Sequence 9796, Ap	1073	222	16.2	234	3	US-08-944-483-56	Sequence 56, Appl
1001	248.5	18.1	717	4	US-09-601-040A-6	Sequence 6, Appl	1074	220.5	16.0	267	2	US-08-978-404B-46	Sequence 46, Appl
1002	248.5	18.1	729	4	US-09-601-040A-2	Sequence 2, Appl	1075	220	16.0	278	4	US-09-270-767-48024	Sequence 48024, A
1003	247.5	18.0	717	4	US-09-601-040A-8	Sequence 8, Appl	1076	220	16.0	457	4	US-09-270-767-32807	Sequence 32807, A
1004	247.5	18.0	729	4	US-09-601-040A-4	Sequence 4, Appl	1077	217.5	15.8	385	4	US-09-163-951-16	Sequence 16, Appl
1005	247	18.0	229	3	US-08-944-483-30	Sequence 30, Appl	1078	217.5	15.8	385	4	US-09-345-881-16	Sequence 16, Appl
1006	245	17.8	226	4	US-09-601-040A-28	Sequence 28, Appl	1079	216	15.7	185	3	US-08-906-769-141	Sequence 141, App
1007	245	17.8	228	2	US-08-766-982-11	Sequence 11, Appl	1080	216	15.7	185	3	US-08-906-616-141	Sequence 141, App
1008	245	17.8	228	3	US-08-944-483-55	Sequence 55, Appl	1081	216	15.7	185	3	US-08-639-075A-141	Sequence 141, App
1009	245	17.8	228	3	US-09-296-219-11	Sequence 11, Appl	1082	216	15.7	185	3	US-09-012-431-141	Sequence 141, App
1010	245	17.8	711	1	US-08-184-012C-8	Sequence 8, Appl	1083	216	15.7	185	3	US-09-012-692-141	Sequence 141, App
1011	245	17.8	711	1	US-08-334-177-2	Sequence 2, Appl	1084	216	15.7	185	3	US-08-906-613-141	Sequence 141, App
1012	245	17.8	711	2	US-08-666-082B-1	Sequence 1, Appl	1085	216	15.7	223	1	US-08-278-091-13	Sequence 13, Appl
1013	245	17.8	711	2	US-08-766-982-2	Sequence 2, Appl	1086	216	15.7	223	1	US-08-483-859-13	Sequence 13, Appl
1014	245	17.8	711	3	US-09-236-219-2	Sequence 2, Appl	1087	216	15.7	223	1	US-08-472-173-13	Sequence 13, Appl
1015	245	17.8	711	4	US-09-600-991-20	Sequence 20, Appl	1088	216	15.7	223	2	US-08-482-816-13	Sequence 13, Appl
1016	245	17.8	711	4	US-09-601-040A-12	Sequence 12, Appl	1089	216	15.7	223	2	US-08-296-149-13	Sequence 13, Appl
1017	245	17.8	711	4	US-09-949-016-6981	Sequence 6981, Ap	1090	216	15.7	223	2	US-08-801-499-13	Sequence 13, Appl
1018	245	17.8	711	5	PCT-US95-13830-2	Sequence 2, Appl	1091	216	15.7	223	2	US-08-615-271-13	Sequence 13, Appl
1019	244.5	17.8	716	2	US-08-766-982-1	Sequence 1, Appl	1092	216	15.7	223	2	US-09-074-660-13	Sequence 13, Appl
1020	244.5	17.8	716	3	US-09-296-219-1	Sequence 1, Appl	1093	216	15.7	223	3	US-09-074-659-13	Sequence 13, Appl
1021	242	17.6	214	6	5180819-3	Patent No. 5180819	1094	216	15.7	223	3	US-09-106-468-13	Sequence 13, Appl
1022	242	17.6	214	6	5180819-3	Patent No. 5180819	1095	216	15.7	223	3	US-09-106-468-13	Sequence 13, Appl
1023	242	17.6	455	3	US-09-261-416-2	Sequence 2, Appl	1096	216	15.7	223	3	US-09-106-468-13	Sequence 13, Appl
1024	240	17.5	161	3	US-09-261-416-8	Sequence 8, Appl	1097	216	15.7	223	1	US-08-485-455D-17	Sequence 17, Appl
1025	234	17.0	158	3	US-09-518-046-22	Sequence 22, Appl	1098	211	15.4	223	1	US-08-485-455D-17	Sequence 17, Appl
1026	232.5	16.9	185	3	US-08-705-875A-5	Sequence 5, Appl	1099	211	15.4	223	2	US-08-482-130C-17	Sequence 17, Appl
1027	232.5	16.9	185	3	US-09-220-731-22	Sequence 22, Appl	1100	211	15.4	223	2	US-08-484-211C-17	Sequence 17, Appl
1028	232.5	16.9	185	4	US-09-242-999-5	Sequence 5, Appl	1101	211	15.4	223	3	US-08-817-795-17	Sequence 17, Appl
1029	231.5	16.8	219	2	US-08-925-708-2	Sequence 2, Appl	1102	211	15.4	223	3	US-08-485-443B-17	Sequence 17, Appl
1030	231	16.8	242	3	US-08-944-483-29	Sequence 29, Appl	1103	211	15.4	223	5	PCT-US95-14442A-17	Sequence 17, Appl
1031	230.5	16.8	304	3	US-09-088-651-2	Sequence 2, Appl	1104	211	15.4	224	3	US-08-906-769-17	Sequence 17, Appl
1032	228.5	16.6	287	4	US-09-270-767-33263	Sequence 33263, A	1105	211	15.4	224	3	US-08-906-616-17	Sequence 17, Appl
1033	228.5	16.6	287	4	US-09-270-767-48480	Sequence 48480, A	1106	211	15.4	224	3	US-08-639-075A-17	Sequence 17, Appl
1034	227	16.5	258	4	US-09-023-942A-8	Sequence 8, Appl	1107	211	15.4	224	3	US-08-817-795-17	Sequence 17, Appl
1035	227	16.5	259	3	US-08-906-769-190	Sequence 190, App	1108	211	15.4	224	3	US-08-485-443B-17	Sequence 17, Appl
1036	227	16.5	259	3	US-08-906-616-190	Sequence 190, App	1109	211	15.4	224	3	US-08-906-769-17	Sequence 17, Appl
1037	227	16.5	259	3	US-08-639-075A-190	Sequence 190, App	1110	211	15.4	224	3	US-08-906-613-17	Sequence 17, Appl
1038	227	16.5	259	3	US-09-004-731-85	Sequence 85, Appl	1111	210.5	15.3	222	4	US-09-796-110-2	Sequence 2, Appl
1039	227	16.5	259	3	US-09-012-431-190	Sequence 190, App	1112	210.5	15.3	228	6	US-08-944-483-31	Sequence 31, Appl
1040	227	16.5	259	3	US-08-749-699-85	Sequence 85, Appl	1113	210.5	15.3	238	6	5180819-4	Patent No. 5180819
1041	227	16.5	259	3	US-09-012-692-190	Sequence 190, App	1114	210.5	15.3	238	6	5180819-4	Patent No. 5180819
1042	227	16.5	259	3	US-08-906-613-190	Sequence 190, App	1115	206	15.0	250	4	US-09-518-046-25	Sequence 23, Appl
1043	227	16.5	259	4	US-09-004-729-85	Sequence 85, Appl	1116	206	15.0	250	4	US-09-518-046-25	Sequence 23, Appl
1044	227	16.5	723	3	US-08-700-519J-18	Sequence 18, Appl	1117	204.5	14.9	157	3	US-08-906-769-107	Sequence 107, App
1045	226.5	16.5	215	6	5180819-2	Patent No. 5180819	1118	204.5	14.9	178	3	US-08-906-616-107	Sequence 107, App
1046	226.5	16.5	215	6	5180819-2	Patent No. 5180819	1119	204.5	14.9	178	3	US-08-906-616-107	Sequence 107, App
1047	226	16.4	697	2	US-08-460-890A-50	Sequence 50, Appl	1120	204.5	14.9	178	3	US-08-817-795-107	Sequence 107, App
1048	226	16.4	697	3	US-08-167-641C-50	Sequence 50, Appl	1121	204.5	14.9	178	3	US-08-639-075A-107	Sequence 107, App
1049	226	16.4	697	3	US-08-460-971A-50	Sequence 50, Appl	1122	204.5	14.9	178	3	US-09-012-431-107	Sequence 107, App

1123	204.5	14.9	178	3	US-09-012-692-107	Sequence 107, App	1196	160.5	11.7	178	3	US-09-220-731-24	Sequence 24, Appl
1124	204.5	14.9	178	3	US-08-906-613-107	Sequence 107, App	1197	160.5	11.7	178	4	US-09-242-999-24	Sequence 24, Appl
1125	204.5	14.9	178	5	PCT-US95-14442A-107	Sequence 107, App	1198	160	11.6	97	4	US-09-270-767-31931	Sequence 31931, A
1126	200.5	14.6	159	3	US-09-518-046-24	Sequence 24, Appl	1199	160	11.6	97	4	US-09-270-767-47148	Sequence 47148, A
1127	200	14.6	223	4	US-09-270-767-45768	Sequence 45768, A	1200	159	11.6	190	2	US-08-845-988-6	Sequence 6, Appl
1128	198.5	14.4	254	3	US-08-906-769-129	Sequence 129, App	1201	159	11.6	190	3	US-09-206-537-6	Sequence 6, Appl
1129	198.5	14.4	254	3	US-08-906-616-129	Sequence 129, App	1202	159	11.6	190	3	US-09-430-854-6	Sequence 6, Appl
1130	198.5	14.4	254	3	US-08-639-075A-129	Sequence 129, App	1203	158	11.5	357	4	US-09-270-767-43564	Sequence 43564, A
1131	198.5	14.4	254	3	US-09-012-431-129	Sequence 129, App	1204	158	11.5	357	4	US-09-270-767-58936	Sequence 58936, A
1132	198.5	14.4	254	3	US-09-012-692-129	Sequence 129, App	1205	157.5	11.5	764	2	US-08-177-109A-2	Sequence 2, Appl
1133	198.5	14.4	254	3	US-08-906-613-129	Sequence 129, App	1206	157.5	11.5	764	2	US-08-687-706-2	Sequence 2, Appl
1134	196.5	14.3	141	4	US-09-949-016-7265	Sequence 7265, App	1207	157.5	11.5	798	4	US-09-949-016-11021	Sequence 11021, A
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1136	195	14.2	326	4	US-10-057-951-3	Sequence 3, Appl	1209	156.5	11.4	163	4	US-09-270-767-60652	Sequence 60652, A
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1138	192.5	14.0	260	3	US-08-906-616-139	Sequence 139, App	1211	156	11.4	112	4	US-09-270-767-33319	Sequence 33319, A
1139	192.5	14.0	260	3	US-08-639-075A-139	Sequence 139, App	1212	156	11.4	112	4	US-09-270-767-48536	Sequence 48536, A
1140	192.5	14.0	260	3	US-09-012-431-139	Sequence 139, App	1213	154.5	11.2	204	3	US-08-906-769-147	Sequence 147, App
1141	192.5	14.0	260	3	US-09-012-692-139	Sequence 139, App	1214	154.5	11.2	204	3	US-08-906-616-147	Sequence 147, App
1142	192.5	14.0	260	3	US-08-906-613-139	Sequence 139, App	1215	154.5	11.2	204	3	US-08-639-075A-147	Sequence 147, App
1143	191	13.9	74	4	US-09-205-258-1151	Sequence 1151, App	1216	154.5	11.2	204	3	US-09-012-431-147	Sequence 147, App
1144	191	13.9	138	6	5200340-4	Patent No. 5200340	1217	154.5	11.2	204	3	US-09-012-692-147	Sequence 147, App
1145	191	13.9	138	6	5200340-4	Patent No. 5200340	1218	154.5	11.2	204	3	US-08-906-613-147	Sequence 147, App
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1152	182	13.2	145	3	US-08-906-616-123	Sequence 123, App	1225	149	10.8	77	3	US-09-352-616A-329	Sequence 329, App
1153	182	13.2	145	3	US-08-639-075A-123	Sequence 123, App	1226	149	10.8	77	4	US-09-232-149A-329	Sequence 329, App
1154	182	13.2	145	3	US-09-012-692-123	Sequence 123, App	1227	149	10.8	77	4	US-09-636-215-329	Sequence 329, App
1155	182	13.2	145	3	US-08-906-613-123	Sequence 123, App	1228	149	10.8	77	4	US-09-685-166A-329	Sequence 329, App
1156	181	13.2	118	4	US-09-621-976-5522	Sequence 5522, App	1229	149	10.8	77	4	US-09-688-489-329	Sequence 329, App
1157	181	13.2	133	4	US-09-949-016-7471	Sequence 7471, App	1230	149	10.8	77	4	US-08-679-426-329	Sequence 329, App
1158	180	13.1	144	3	US-09-012-431-123	Sequence 123, App	1231	149	10.8	77	4	US-09-759-143-329	Sequence 329, App
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1160	178.5	13.0	164	3	US-09-030-607-178	Sequence 178, App	1233	148.5	10.8	276	4	US-09-270-767-32048	Sequence 32048, A
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1171	178.5	13.0	164	4	US-09-651-236-178	Sequence 178, App	1244	142.5	10.4	208	3	US-08-906-616-151	Sequence 151, App
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1179	168	12.2	141	3	US-09-012-431-135	Sequence 135, App	1252	139	10.1	87	3	US-08-906-616-161	Sequence 161, App
1180	168	12.2	141	3	US-09-012-692-135	Sequence 135, App	1253	139	10.1	87	3	US-08-639-075A-161	Sequence 161, App
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1183	166.5	12.1	178	3	US-09-220-731-23	Sequence 23, Appl	1256	139	10.1	87	3	US-08-906-613-161	Sequence 161, App
1184	166.5	12.1	178	4	US-09-242-999-8	Sequence 8, Appl	1257	139	10.1	89	3	US-08-906-769-165	Sequence 165, App
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1188	165	12.0	198	3	US-08-906-616-133	Sequence 133, App	1261	139	10.1	89	3	US-09-012-692-165	Sequence 165, App
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1191	165	12.0	198	3	US-09-012-692-133	Sequence 133, App	1264	134	9.8	203	4	US-09-270-767-32531	Sequence 32531, A
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1194	163	11.9	190	3	US-09-206-537-4	Sequence 4, Appl	1267	128	9.3	246	4	US-09-370-838-60	Sequence 60, Appl
1195	163	11.9	190	3	US-09-430-854-4	Sequence 4, Appl	1268	128	9.3	246	4	US-09-854-133-60	Sequence 60, Appl

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1271	126	9.2	142	3	US-08-906-769-155	Sequence 155, App	1344	115.5	8.4	138	4	US-09-270-767-32323	Sequence 32323, A
1272	126	9.2	142	3	US-08-906-616-155	Sequence 155, App	1345	115.5	8.4	138	4	US-09-270-767-47540	Sequence 47540, A
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1274	126	9.2	142	3	US-09-004-731-83	Sequence 83, Appl	1347	115	8.4	80	2	US-08-482-130C-69	Sequence 69, Appl
1275	126	9.2	142	3	US-09-012-431-155	Sequence 155, App	1348	115	8.4	80	2	US-08-484-211C-69	Sequence 69, Appl
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1278	126	9.2	142	3	US-08-906-613-155	Sequence 155, App	1351	113	8.2	137	4	US-09-270-767-61091	Sequence 61091, A
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1282	124	9.0	125	3	US-08-817-795-97	Sequence 97, Appl	1355	112	8.2	80	3	US-08-485-443B-69	Sequence 69, Appl
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1286	124	9.0	125	3	US-08-906-613-97	Sequence 97, Appl	1359	112	8.2	80	3	US-08-906-613-69	Sequence 69, Appl
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1293	121.5	8.8	86	2	US-08-484-211C-53	Sequence 53, Appl	1366	110.5	8.0	99	3	US-08-639-075A-93	Sequence 93, Appl
1294	121.5	8.8	86	3	US-08-906-769-53	Sequence 53, Appl	1367	110.5	8.0	99	3	US-09-012-431-93	Sequence 93, Appl
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1296	121.5	8.8	86	3	US-08-906-616-53	Sequence 53, Appl	1369	110.5	8.0	99	3	US-08-906-613-93	Sequence 93, Appl
1297	121.5	8.8	86	3	US-08-817-795-53	Sequence 53, Appl	1370	110.5	8.0	99	5	PCT-US95-14442A-93	Sequence 93, Appl
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1299	121.5	8.8	86	3	US-08-639-075A-53	Sequence 53, Appl	1372	109.5	8.0	33	3	US-08-944-483-27	Sequence 27, Appl
1300	121.5	8.8	86	3	US-09-012-431-53	Sequence 53, Appl	1373	107	7.8	187	4	US-09-270-767-43542	Sequence 43542, A
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1302	121.5	8.8	86	5	PCT-US95-14442A-53	Sequence 53, Appl	1375	105.5	7.7	36	3	US-08-944-483-26	Sequence 26, Appl
1303	120.5	8.8	45	3	US-09-070-526-4	Sequence 53, Appl	1376	105.5	7.7	97	4	US-09-270-767-32342	Sequence 32342, A
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1306	120	8.7	130	2	US-08-484-211C-67	Sequence 67, Appl	1379	105.5	7.7	136	3	US-08-906-616-137	Sequence 137, App
1307	120	8.7	130	3	US-08-906-769-67	Sequence 67, Appl	1380	105.5	7.7	136	3	US-08-639-075A-137	Sequence 137, App
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1310	120	8.7	130	3	US-08-485-443B-67	Sequence 67, Appl	1383	105.5	7.7	136	3	US-08-749-699-79	Sequence 79, Appl
1311	120	8.7	130	3	US-08-639-075A-67	Sequence 67, Appl	1384	105.5	7.7	136	3	US-09-012-692-137	Sequence 137, App
1312	120	8.7	130	3	US-09-012-431-67	Sequence 67, Appl	1385	105.5	7.7	136	3	US-08-906-613-137	Sequence 137, App
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1317	119	8.7	97	2	US-08-482-130C-63	Sequence 63, Appl	1390	102.5	7.5	80	2	US-08-484-211C-59	Sequence 59, Appl
1318	119	8.7	97	2	US-08-484-211C-63	Sequence 63, Appl	1391	102.5	7.5	80	3	US-08-906-769-59	Sequence 59, Appl
1319	119	8.7	97	3	US-08-906-769-63	Sequence 63, Appl	1392	102.5	7.5	80	3	US-08-906-616-59	Sequence 59, Appl
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1321	119	8.7	97	3	US-08-817-795-63	Sequence 63, Appl	1394	102.5	7.5	80	3	US-08-485-443B-59	Sequence 59, Appl
1322	119	8.7	97	3	US-08-485-443B-63	Sequence 63, Appl	1395	102.5	7.5	80	3	US-08-639-075A-59	Sequence 59, Appl
1323	119	8.7	97	3	US-08-639-075A-63	Sequence 63, Appl	1396	102.5	7.5	80	3	US-09-012-431-59	Sequence 59, Appl
1324	119	8.7	97	3	US-09-012-431-63	Sequence 63, Appl	1397	102.5	7.5	80	3	US-09-012-692-59	Sequence 59, Appl
1325	119	8.7	97	3	US-09-012-692-63	Sequence 63, Appl	1398	102.5	7.5	80	3	US-08-906-613-59	Sequence 59, Appl
1326	119	8.7	97	3	US-08-906-613-63	Sequence 63, Appl	1399	102.5	7.5	80	5	PCT-US95-14442A-59	Sequence 59, Appl
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1330	118	8.6	130	3	US-08-639-075A-157	Sequence 157, App	1403	101	7.4	125	4	US-09-270-767-48219	Sequence 48219, A
1331	118	8.6	130	3	US-09-012-431-157	Sequence 157, App	1404	101	7.4	339	4	US-09-543-681A-6965	Sequence 6965, Ap
1332	118	8.6	130	3	US-09-012-692-157	Sequence 157, App	1405	100.5	7.3	55	4	US-08-843-076D-22	Sequence 22, Appl
1333	118	8.6	130	3	US-08-906-613-157	Sequence 157, App	1406	100	7.3	68	1	US-08-485-455D-77	Sequence 77, Appl
1334	117.5	8.6	144	3	US-08-906-769-153	Sequence 153, App	1407	100	7.3	68	2	US-08-482-130C-77	Sequence 77, Appl
1335	117.5	8.6	144	3	US-08-906-616-153	Sequence 153, App	1408	100	7.3	68	2	US-08-484-211C-77	Sequence 77, Appl
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1338	117.5	8.6	144	3	US-09-012-431-153	Sequence 153, App	1411	100	7.3	68	3	US-08-817-795-77	Sequence 77, Appl
1339	117.5	8.6	144	3	US-08-749-699-81	Sequence 81, Appl	1412	100	7.3	68	3	US-08-485-443B-77	Sequence 77, Appl
1340	117.5	8.6	144	3	US-09-012-692-153	Sequence 153, App	1413	100	7.3	68	3	US-08-639-075A-77	Sequence 77, Appl
1341	117.5	8.6	144	3	US-08-906-613-153	Sequence 153, App	1414	100	7.3	68	3	US-09-012-431-77	Sequence 77, Appl

1415	100	7.3	68	3	US-09-012-692-77	Sequence 77, Appl	1488	88	6.4	102	3	US-08-639-075A-125	Sequence 125, App
1416	100	7.3	68	3	US-08-906-613-77	Sequence 77, Appl	1489	88	6.4	102	3	US-09-012-431-125	Sequence 125, App
1417	100	7.3	68	5	PCT-US95-14442A-77	Sequence 77, Appl	1490	88	6.4	102	3	US-09-012-692-125	Sequence 125, App
1418	100	7.3	69	3	US-08-906-769-101	Sequence 101, App	1491	88	6.4	102	3	US-08-906-613-125	Sequence 125, App
1419	100	7.3	69	3	US-08-906-616-101	Sequence 101, App	1492	88	6.4	238	4	US-09-270-767-44825	Sequence 44825, A
1420	100	7.3	69	3	US-08-817-795-101	Sequence 101, App	1493	87.5	6.4	64	1	US-08-485-455D-75	Sequence 75, Appl
1421	100	7.3	69	3	US-08-639-075A-101	Sequence 101, App	1494	87.5	6.4	64	2	US-08-482-130C-75	Sequence 75, Appl
1422	100	7.3	69	3	US-09-012-431-101	Sequence 101, App	1495	87.5	6.4	64	2	US-08-484-211C-75	Sequence 75, Appl
1423	100	7.3	69	3	US-09-012-692-101	Sequence 101, App	1496	87.5	6.4	64	3	US-08-906-769-75	Sequence 75, Appl
1424	100	7.3	69	3	US-08-906-613-101	Sequence 101, App	1497	87.5	6.4	64	3	US-08-906-616-75	Sequence 75, Appl
1425	100	7.3	69	5	PCT-US95-14442A-101	Sequence 101, App	1498	87.5	6.4	64	3	US-08-817-795-75	Sequence 75, Appl
1426	99.5	7.2	84	3	US-08-906-769-99	Sequence 99, Appl	1499	87.5	6.4	64	3	US-08-485-443B-75	Sequence 75, Appl
1427	99.5	7.2	84	3	US-08-906-616-99	Sequence 99, Appl	1500	87.5	6.4	64	3	US-08-639-075A-75	Sequence 75, Appl
1428	99.5	7.2	84	3	US-08-817-795-99	Sequence 99, Appl							
1429	99.5	7.2	84	3	US-08-639-075A-99	Sequence 99, Appl							
1430	99.5	7.2	84	3	US-09-012-431-99	Sequence 99, Appl							
1431	99.5	7.2	84	3	US-09-012-692-99	Sequence 99, Appl							
1432	99.5	7.2	84	3	US-08-906-613-99	Sequence 99, Appl							
1433	99.5	7.2	84	5	PCT-US95-14442A-99	Sequence 99, Appl							
1434	99.5	7.2	146	4	US-09-270-767-43546	Sequence 43546, A							
1435	99	7.2	50	1	US-07-666-913A-2	Sequence 2, Appl							
1436	98.5	7.2	128	3	US-08-906-769-143	Sequence 143, App							
1437	98.5	7.2	128	3	US-08-906-616-143	Sequence 143, App							
1438	98.5	7.2	128	3	US-08-639-075A-143	Sequence 143, App							
1439	98.5	7.2	128	3	US-09-012-431-143	Sequence 143, App							
1440	98.5	7.2	128	3	US-09-012-692-143	Sequence 143, App							
1441	98.5	7.2	128	3	US-08-906-613-143	Sequence 143, App							
1442	97.5	7.1	108	4	US-09-270-767-33364	Sequence 33364, A							
1443	97.5	7.1	142	3	US-09-004-731-38	Sequence 38, Appl							
1444	97.5	7.1	142	3	US-08-749-699-38	Sequence 38, Appl							
1445	97.5	7.1	142	4	US-09-004-729-38	Sequence 38, Appl							
1446	97.5	7.1	149	4	US-09-270-767-46053	Sequence 46053, A							
1447	97	7.0	639	2	US-08-637-899-1	Sequence 1, Appl							
1448	96	7.0	93	4	US-09-621-976-4137	Sequence 4137, Ap							
1449	95	6.9	332	4	US-09-602-777A-42	Sequence 42, Appl							
1450	94.5	6.9	102	4	US-09-270-767-58913	Sequence 58913, A							
1451	94.5	6.9	109	3	US-08-906-769-109	Sequence 109, App							
1452	94.5	6.9	119	3	US-08-906-616-109	Sequence 109, App							
1453	94.5	6.9	119	3	US-08-817-795-109	Sequence 109, App							
1454	94.5	6.9	119	3	US-08-639-075A-109	Sequence 109, App							
1455	94.5	6.9	119	3	US-09-012-431-109	Sequence 109, App							
1456	94.5	6.9	119	3	US-09-012-692-109	Sequence 109, App							
1457	94.5	6.9	119	3	US-08-906-613-109	Sequence 109, App							
1458	94.5	6.9	119	5	PCT-US95-14442A-109	Sequence 109, App							
1459	93.5	6.8	123	4	US-09-949-016-9268	Sequence 9268, Ap							
1460	93.5	6.8	185	1	US-08-278-091-14	Sequence 14, Appl							
1461	93.5	6.8	185	1	US-08-483-859-14	Sequence 14, Appl							
1462	93.5	6.8	185	1	US-08-472-173-14	Sequence 14, Appl							
1463	93.5	6.8	185	2	US-08-487-167-14	Sequence 14, Appl							
1464	93.5	6.8	185	2	US-08-482-816-14	Sequence 14, Appl							
1465	93.5	6.8	185	2	US-08-296-149-14	Sequence 14, Appl							
1466	93.5	6.8	185	2	US-08-801-499-14	Sequence 14, Appl							
1467	93.5	6.8	185	2	US-08-615-271-14	Sequence 14, Appl							
1468	93.5	6.8	185	3	US-09-074-659-14	Sequence 14, Appl							
1469	93.5	6.8	185	3	US-09-106-468-14	Sequence 14, Appl							
1470	93.5	6.8	185	3	US-09-106-468-14	Sequence 14, Appl							
1471	93.5	6.8	185	3	US-09-106-466A-14	Sequence 14, Appl							
1472	93.5	6.8	185	3	US-09-106-467-14	Sequence 14, Appl							
1473	93.5	6.8	185	6	5514590-10	Patent No. 5514590							
1474	93.5	6.8	185	6	5514590-10	Patent No. 5514590							
1475	93.5	6.8	299	6	5514590-4	Patent No. 5514590							
1476	93.5	6.8	299	6	5514590-4	Patent No. 5514590							
1477	93	6.8	220	4	US-09-270-767-42857	Sequence 42857, A							
1478	90	6.6	42	1	US-08-293-778-11	Sequence 11, Appl							
1479	90	6.6	163	4	US-09-270-767-32837	Sequence 32837, A							
1480	89.5	6.5	501	4	US-09-252-991A-19191	Sequence 19191, A							
1481	89.5	6.5	3594	4	US-09-911-842A-4	Sequence 4, Appl							
1482	89	6.5	294	3	US-09-518-046-4	Sequence 4, Appl							
1483	88.5	6.4	1935	4	US-09-949-016-10403	Sequence 10403, A							
1484	88.5	6.4	2205	1	US-08-093-453B-2	Sequence 2, Appl							
1485	88	6.4	52	4	US-08-270-767-59783	Sequence 59783, A							
1486	88	6.4	102	3	US-08-906-769-125	Sequence 125, App							
1487	88	6.4	102	3	US-08-906-616-125	Sequence 125, App							

ALIGNMENTS

RESULT 1  
US-09-949-016-8151  
; Sequence 8151, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CLO01307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 8151  
; LENGTH: 249  
; TYPE: PRT  
; ORGANISM: Human  
; US-09-949-016-8151

Query Match 98.9%; Score 1359.5; DB 4; Length 249;  
Best Local Similarity 99.6%; Pred. No. 3.1e-124;  
Matches 247; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy	1	MGLSIFLLLCVLGLSQAATPKIFNGTCGRNSQPWQVGLFEGTSLRCGGVLIDHRWLTA	60
Db	3	MGLSIFLLLCVLGLSQAATPKIFNGTCGRNSQPWQVGLFEGTSLRCGGVLIDHRWLTA	62
Qy	61	AHCSGSRYWRLGHSLSOLDWTEQIRHSGFSVTHPGVLGASTSHEHDLRLRLPVRV	120
Db	63	AHCSG-RYWRLGHSLSQLDWTQIRHSGFSVTHPGVLGASTSHEHDLRLRLPVRV	121
Qy	121	TSSVQPLPLPNDCATAGTCHVSGWGTNNPRNPPDLLQCLNLSIVSHATCHGVYPGRI	180
Db	122	TSSVQPLPLPNDCATAGTCHVSGWGTNNPRNPPDLLQCLNLSIVSHATCHGVYPGRI	181
Qy	181	TSNNVACAGVPQDACCGDSGLPVCQGLVQGLVSWGSGVPCGQDGPVGYVYCKYVDW	240
Db	182	TSNNVACAGVPQDACCGDSGLPVCQGLVQGLVSWGSGVPCGQDGPVGYVYCKYVDW	241
Qy	241	IRIMIMRNN	248
Db	242	IRIMIMRNN	249

RESULT 2  
US-09-949-016-6948  
; Sequence 6948, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.  
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
FILE REFERENCE: CL001307  
CURRENT FILING DATE: 2000-04-14  
PRIORITY APPLICATION NUMBER: 60/241,755  
PRIORITY FILING DATE: 2000-10-20  
PRIORITY APPLICATION NUMBER: 60/237,768  
PRIORITY FILING DATE: 2000-10-03  
PRIORITY APPLICATION NUMBER: 60/231,498  
PRIORITY FILING DATE: 2000-09-08  
NUMBER OF SEQ ID NOS: 207012  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 6948  
LENGTH: 254  
TYPE: PRT  
ORGANISM: Human  
US-09-949-016-6948

Query Match 94.7%; Score 1301; DB 4; Length 254;  
Best Local Similarity 100.0%; Pred. No. 1.5e-118;  
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MGLSIFLLCVLGSQAATPKIFNGTECGRNSQPWQVGLFEGTSLRCGGVLIDHRWLTA 60  
DB 1 MGLSIFLLCVLGSQAATPKIFNGTECGRNSQPWQVGLFEGTSLRCGGVLIDHRWLTA 60  
QY 61 AHCSGSRYWRLGHSLSQLDWTQIRHSGFSVTHPGYLGASTSHEHDLRLRLRPV 120  
DB 61 AHCSGSRYWRLGHSLSQLDWTQIRHSGFSVTHPGYLGASTSHEHDLRLRLRPV 120  
QY 121 TSSVQPLPLNDCATAGTECHVSGWGTINHPRPDPDLLOCLNLSIVSHATCHGVYPGRI 180  
DB 121 TSSVQPLPLNDCATAGTECHVSGWGTINHPRPDPDLLOCLNLSIVSHATCHGVYPGRI 180  
QY 181 TSNMVCAGVPGQDACQDGGPLVCGVQLGVLVSGVSGPCGQDGIPIGVYTYIC 235  
DB 181 TSNMVCAGVPGQDACQDGGPLVCGVQLGVLVSGVSGPCGQDGIPIGVYTYIC 235

RESULT 3  
US-09-244-111-6  
Sequence 6, Application US/09244111  
Patent No. 6566498  
GENERAL INFORMATION:  
APPLICANT: Ni, et al.  
TITLE OF INVENTION: Human Serine Protease and Serpin Polypeptides  
FILE REFERENCE: PF391  
CURRENT APPLICATION NUMBER: US/09/244,111  
CURRENT FILING DATE: 1999-02-04  
EARLIER APPLICATION NUMBER: 60/073,961  
EARLIER FILING DATE: 1998-02-06  
NUMBER OF SEQ ID NOS: 13  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 6  
LENGTH: 162  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-244-111-6

Query Match 59.0%; Score 811; DB 4; Length 162;  
Best Local Similarity 64.1%; Pred. No. 3.8e-71;  
Matches 159; Conservative 0; Mismatches 3; Indels 86; Gaps 3;  
QY 1 MGLSIFLLCVLGSQAATPKIFNGTECGRNSQPWQVGLFEGTSLRCGGVLIDHRWLTA 60  
DB 1 MGLSIFLLCVLGSQAATPKIFNGTECGRNSQPWQVGLFEGTSLRCGGVLIDHRWLTA 60  
QY 61 AHCSGSRYWRLGHSLSQLDWTQIRHSGFSVTHPGYLGASTSHEHDLRLRLRPV 120  
DB 61 AH-----WQRO-----THIS----- 69

QY 121 TSSVQPLPLNDCATAGTECHVSGWGTINHPRPDPDLLOCLNLSIVSHATCHGVYPGRI 180  
DB 70 -----PDLLOCLNLSIVSHATCHGVYPGRI 94  
QY 181 TSNMVCAGVPGQDACQDGGPLVCGVQLGVLVSGVSGPCGQDGIPIGVYTYIC 240  
DB 95 TSNMVCAGVPGQDACQDGGPLVCGVQLGVLVSGVSGPCGQDGIPIGVYTYIC 154  
QY 241 IRMIMENN 248  
DB 155 IRMIMENN 162

RESULT 4  
US-09-618-259-7  
Sequence 7, Application US/09618259  
Patent No. 6642013  
GENERAL INFORMATION:  
APPLICANT: O'Brien, Timothy J.  
APPLICANT: Underwood, Timothy J.  
TITLE OF INVENTION: No. 6642013el Extracellular Serine Protease  
FILE REFERENCE: D6020CIP2  
CURRENT APPLICATION NUMBER: US/09/618,259  
CURRENT FILING DATE: 2000-07-18  
PRIORITY APPLICATION NUMBER: US 09/127,444  
PRIORITY FILING DATE: 1998-08-21  
NUMBER OF SEQ ID NOS: 72  
SEQ ID NO 7  
LENGTH: 260  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: Amino acid sequence of TADG-14 protein  
US-09-618-259-7

Query Match 45.9%; Score 630.5; DB 4; Length 260;  
Best Local Similarity 50.2%; Pred. No. 2.5e-53;  
Matches 123; Conservative 24; Mismatches 93; Indels 5; Gaps 3;  
QY 5 IFLL-----CVLGLSQAATPKIFNGTECGRNSQPWQVGLFEGTSLRCGGVLIDHRWLTA 61  
DB 13 MFLLLGGAWAGHSAQEDKVLGHECQHSQPWQAALFOGQQLCCGVLVGGNWLTA 72  
QY 62 HCSGSRYWRLGHSLSQLDWTQIRHSGFSVTHPGYLGAST-SHEHDLRLRLRPV 120  
DB 73 HCKPKYTVLGDHSLQNKDGPQEIIPVQSIHPHCYNSSDVEDHNDMLLQLRDOASL 132  
QY 121 TSSVQPLPLNDCATAGTECHVSGWGTINHPRPDPDLLOCLNLSIVSHATCHGVYPGRI 180  
DB 133 GSKVKPTISLADHCTQPGQKCTVSGWGTVPSPRENFPDTLNCAEVKIPFQKKCEDAYPGQI 192  
QY 181 TSNMVCAGVPGQDACQDGGPLVCGVQLGVLVSGVSGPCGQDGIPIGVYTYIC 240  
DB 193 TDGMVCAGSSKGADTCQDSSGGPLVCDGALQGITSWGSDPCGSRDFGVYTYIC 251  
QY 241 IRMIM 245  
DB 252 IKKII 256

RESULT 5  
US-09-070-526-2  
Sequence 2, Application US/09070526  
Patent No. 6100059  
GENERAL INFORMATION:  
APPLICANT: SOUTHAN, CHRISTOPHER  
APPLICANT: CLINKENBEARD, HELEN  
APPLICANT: BURGESS, NICOLA  
TITLE OF INVENTION: No. 6100059el Compounds  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: RATNER & PRESTIA  
STREET: P.O. BOX 980



CITY: VALLEY FORGE  
STATE: PA  
COUNTRY: USA  
ZIP: 19482  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/070,526  
FILING DATE: 30-APR-1998  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 9711952.3  
FILING DATE: 9-JUN-1997  
APPLICATION NUMBER: EP 97309646.4  
FILING DATE: 1-DEC-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: PRESTIA, PAUL F  
REGISTRATION NUMBER: 23,031  
REFERENCE/DOCKET NUMBER: GH-30353  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 610-407-0700  
TELEFAX: 610-407-0701  
TELEX: 846169  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 260 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-070-526-2

Query Match 45.6%; Score 626.5; DB 3; Length 260;

Best Local Similarity 50.4%; Pred. No. 6.2e-53;

Matches 122; Conservative 23; Mismatches 92; Indels 5; Gaps 3;

QY 5 IFLLL---CVLGSQAATPKIFNGTCGRNSQPWQVGLFEGTSLRCGVLIDHRWVLTAA 61  
DB 13 MFLLLGGAWAGHRAQEDKVLGHECQPHSQPQAAALFQQQLLCGVLGGNNVLTAA 72  
QY 62 HCSGSRYWVRIGHSLSQLDWTEQIRHSGFSVTHPGYLGAAT-SHEHDLRLRLRLPVRV 120  
DB 73 HCKPKYTVRLGDHSLQKDGPEQIIPWQSIPIPCYNSSDVEDHNDMLQLRDOASL 132  
QY 121 TSSVQPLPLNDCAATAGTECHVSGWGTNHPNPPDLLQCLNLSIVSHATCHGVYPGRI 180  
DB 133 GSKYKPISLADHCTQPGQKCTVSGWGTVTSPPNFPDPLNCAEVKIPFQKKCEDAYPGQI 192  
QY 181 TSNMVCAGGVPQDACOGDSGGLVCGVLGWSVGPVCGODGIPGVVYICKYVDW 240  
DB 193 TDGMVAGSSKGADTCQDGGPLVCDGALQGITWSGS-DPCGRSDKPGVTNLCRYLDD 251  
QY 241 IR 242  
DB 252 IK 253

## RESULT 6

US-09-025-059-3

; Sequence 3, Application US/09025059

; Patent No. 6075136

; GENERAL INFORMATION:

; APPLICANT: Tang, Y. Tom

; APPLICANT: Corley, Neil C.

; APPLICANT: Guegler, Karl J.

; TITLE OF INVENTION: PROSTATE-ASSOCIATED SERINE PROTEASE

; NUMBER OF SEQUENCES: 4

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Incyte Pharmaceuticals, Inc.

; STREET: 3174 Porter Dr.

CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/025,059  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Billings, Lucy J  
REGISTRATION NUMBER: 36,749  
REFERENCE/DOCKET NUMBER: PF-0481 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-855-0555  
TELEFAX: 650-845-4166  
TELEX:  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 260 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
LIBRARY: GenBank  
CLONE: 1020091  
US-09-025-059-3

Query Match 45.3%; Score 622.5; DB 3; Length 260;

Best Local Similarity 49.0%; Pred. No. 1.5e-52;

Matches 121; Conservative 28; Mismatches 93; Indels 5; Gaps 3;

QY 5 IFLLL---LGLSQAATPKIFNGTCGRNSQPWQVGLFEGTSLRCGVLIDHRWVLTAA 61  
DB 13 LLLLFMGAWAGLTAAGSKLEGRECIPIHSQPWQAAALFQGERLICGVLGDRWVLTAA 72  
QY 62 HCSGSRYWVRIGHSLSQLDWTEQIRHSGFSVTHPGYLGAAT-TSHEHDLRLRLRLPVRV 120  
DB 73 HCKKQKYSVRLGDHSLQSRDQPEQEIQVAQSIQHPCTNNSPEDHSDIMLIRLQNSANL 132  
QY 121 TSSVQPLPLNDCAATAGTECHVSGWGTNHPNPPDLLQCLNLSIVSHATCHGVYPGRI 180  
DB 133 GDKVKPYQLANLCPKVQKQCIISGWGTVTSPPNFPNLTNCAEVKIYSONKCEAYPGKI 192  
QY 181 TSNMVCAGGVPQDACOGDSGGLVCGVLGWSVGPVCGODGIPGVVYICKYVDW 240  
DB 193 TEGMVCAGSSNGADTCQDGGPLVCDGMLQGITWSGS-DPCGKPEKPGVTIKICRYTTW 251  
QY 241 IRIMRN 247  
DB 252 IKKTMN 258

## RESULT 7

US-09-008-271A-7

; Sequence 7, Application US/09008271A

; Patent No. 6203979

; GENERAL INFORMATION:

; APPLICANT: Bandman, Olga

; Hillman, Jennifer L.

; Yue, Henry

; Guegler, Karl J.

; Corley, Neil C.

; Tang, Tom Y.

; Shah, Purvi

; TITLE OF INVENTION: HUMAN PROTEASE MOLECULES

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;
;
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Inocyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Dr.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/008,271A
; FILING DATE: 16-Jan-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: <Unknown>
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Mohan-Peterson, Sheila
; REGISTRATION NUMBER: 41,201
; REFERENCE/DOCKET NUMBER: PF-0458 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 260 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: COLNOT27
; CLONE: 1798496
; SEQUENCE DESCRIPTION: SEQ ID NO: 7 :
US-09-008-271A-7

Query Match 45.3%; Score 622.5; DB 3; Length 260;
Best Local Similarity 49.8%; Pred. No. 1.5e-52;
Matches 122; Conservative 24; Mismatches 94; Indels 5; Gaps 3;

Qy 5 IFLLLV---CVLGLSQAATPKIFNGTECGRNSQPQVGLFEGTSLRCGGVLIDHRWLTAA 61
Db 13 MFLLLGGAWAGHSRAQEDKVLGGHECQPHSQPQAAALSQGQLLCGGVLVGGNWLTAA 72

Qy 62 HCSGSRYWVRLGHSLSQLDWTQIRHSGFSVTHPGYLGAST-SHEHDLRLRLRPVRV 120
Db 73 HCKPKYTVRLGHSLSQLDWTQIRHSGFSVTHPGYLGAST-SHEHDLRLRLRLQDQSL 132

Qy 121 TSSVQPLPLPNDCATAGTECHVSGWGITNHPNPFDPDLLOCLNLSIVSHATCHGVYPGRI 180
Db 133 GSKVKPISLADHCTQPGQKCTVSGWGVTSFRENFPDNLNCAEVKIIPQKKCEDAYPGQI 192

Qy 181 TSNMVCAGVPGQDACQDGGSLVCGVQLGVLVSGSVGPGCGDGIPIGVYTYICKYVDW 240
Db 193 TDGMVCAAGSKGATCQDGGSLVCGVQLGVLVSGSVGPGCGDGIPIGVYTYICKYVDW 251

Qy 241 IRMIM 245
Db 252 IKKII 256

RESULT 8
US-09-618-259-8
; Sequence 8, Application US/09618259
; Patent No. 6642013
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; TITLE OF INVENTION: No. 6642013el Extracellular Serine Protease
; FILE REFERENCE: D6020CIP2
; CURRENT APPLICATION NUMBER: US/09/618,259

;
;
; CURRENT FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: US 09/127,444
; FILING DATE: 1998-08-21
; NUMBER OF SEQ ID NOS: 72
; SEQ ID NO 8
; LENGTH: 260
; TYPE: PRT
; ORGANISM: Mus sp.
; FEATURE:
; OTHER INFORMATION: Amino acid sequence of mouse neuropsin homologous
; OTHER INFORMATION: to TADG-14; accession no. D30785
US-09-618-259-8

Query Match 45.3%; Score 622.5; DB 4; Length 260;
Best Local Similarity 49.0%; Pred. No. 1.5e-52;
Matches 121; Conservative 28; Mismatches 93; Indels 5; Gaps 3;

Qy 5 IFLLLV---LGLSQAATPKIFNGTECGRNSQPQVGLFEGTSLRCGGVLIDHRWLTAA 61
Db 13 ILLLLFMGAWAGLTRAQGSKILEGECIPHSQPWQAALFQGERLICGVLVGDRLWLTAA 72

Qy 62 HCSGSRYWVRLGHSLSQLDWTQIRHSGFSVTHPGYLGAS-TSHEHDLRLRLRPVRV 120
Db 73 HCKQKYSVRLGHSLSQLDWTQIRHSGFSVTHPGYLGAS-TSHEHDLRLRLRLQNSANL 132

Qy 121 TSSVQPLPLPNDCATAGTECHVSGWGITNHPNPFDPDLLOCLNLSIVSHATCHGVYPGRI 180
Db 133 GSKVKPVLANLCPKVGQKCIISGWGVTSFQENFNTLNCAEVKIYSONKCEAYPGKI 192

Qy 181 TSNMVCAGVPGQDACQDGGSLVCGVQLGVLVSGSVGPGCGDGIPIGVYTYICKYVDW 240
Db 193 TEGMVCAGSSNGADTCQDGGSLVCGVQLGVLVSGSVGPGCGDGIPIGVYTYICKYVDW 251

Qy 241 IRMIMRN 247
Db 252 IKKTMND 258

RESULT 9
US-09-205-258-427
; Sequence 427, Application US/09205258
; Patent No. 6525174
; GENERAL INFORMATION:
; APPLICANT: Young et al.
; TITLE OF INVENTION: 207 Human Secreted Proteins
; FILE REFERENCE: P2007P1
; CURRENT APPLICATION NUMBER: US/09/205,258
; CURRENT FILING DATE: 1998-12-04
; EARLIER APPLICATION NUMBER: PCT/US98/11422
; EARLIER FILING DATE: 1998-06-04
; EARLIER APPLICATION NUMBER: 60/048,885
; EARLIER FILING DATE: 1997-06-05
; EARLIER APPLICATION NUMBER: 60/049,375
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,881
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,880
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,896
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,020
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,876
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,895
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,884
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,894
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,971
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,964
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Db 95 CLKPRYIVHLQHNKKEGCEQTRTATESFPHPGFNNSLPNKDHNDIMLVKMASPVSI 154  
QY 121 TSSVOPLPLPNDCACTAGTECHVSGWITNHPNPPDLPDLOCLNLSIVSHATCHGVYPGRI 180  
Db 155 TWAVRPLTSSRCVTAGTSCLSISGWTSSPQLRPLHLCANITIIHOKCENAYPGNI 214  
QY 181 TSNMVCAG-GVPGDAGCGGGLVCGGLVGLVSGVSGVPCQDGPVYVYICKYVD 239  
Db 215 TDTMVCASVGEKSDSCGDSGGLVNCQSLQIISWGQ-DPCAITRKPGVYVYICKYVD 273  
QY 240 WIRMIMNN 248  
Db 274 WIQETMKN 282

## RESULT 11

US-09-386-642-13  
; Sequence 13, Application US/09386642  
; Patent No. 6420157  
; GENERAL INFORMATION:  
; APPLICANT: Darrow, Andrew  
; APPLICANT: Qi, Jensen  
; APPLICANT: Andrade-Gordon, Patricia  
; TITLE OF INVENTION: Zymogen Activation System  
; FILE REFERENCE: ORT-1028  
; CURRENT APPLICATION NUMBER: US/09/386,642  
; CURRENT FILING DATE: 1999-08-31  
; NUMBER OF SEQ ID NOS: 60  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 13  
; LENGTH: 288  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Fusion gene  
; OTHER INFORMATION: with homo sapien serine protease catalytic domain  
US-09-386-642-13

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Best Local Similarity 51.1%; Pred. No. 1.5e-50;  
Matches 116; Conservative 21; Mismatches 87; Indels 3; Gaps 3;  
QY 21 KIFNGTEC-GRNSQPMQVGLFEGTSLRCGGVLDHRWLVTAACHGSGRYVRLGEHLSQ 79  
Db 51 KIVGYNCLPSPQWQAALFQGGQLCGVLGVGNVWLVTAACHCKPKYVRLGDHSLQN 110  
QY 80 LDWTEQIRHSGFVTHPGYLGAST-SHEHDLRLRLPLRVVTSSVQPLPLPNDCACTAGT 138  
Db 111 KDGPEQIPVVSIPHPFCYNSDDVEDHNDMLLQLRDLQASLGSKVKPISLADHCTQPGQ 170  
QY 139 ECHVSGWGITNHPNPPDLPDLOCLNLSIVSHATCHGVYVPGRTITSNMVCAGVPGDAGCG 198  
Db 171 KCTVSGWGTVPSPRENPFDTLNCALVKIFPKCKCEDAYPGQITDGMVCAGSSKGADTCQG 230  
QY 199 DSGGGLVCGGLVGLVSGVSGVPCQDGPVYVYICKYVDWIRMIM 245  
Db 231 DSGGGLVCDGALQGITSMGS-DPCGRSKDPGVYVYICKYLDWIKII 276

## RESULT 12

US-09-386-642-14  
; Sequence 14, Application US/09386642  
; Patent No. 6420157  
; GENERAL INFORMATION:  
; APPLICANT: Darrow, Andrew  
; APPLICANT: Qi, Jensen  
; APPLICANT: Andrade-Gordon, Patricia  
; TITLE OF INVENTION: Zymogen Activation System  
; FILE REFERENCE: ORT-1028  
; CURRENT APPLICATION NUMBER: US/09/386,642  
; CURRENT FILING DATE: 1999-08-31  
; NUMBER OF SEQ ID NOS: 60  
; SOFTWARE: Patentin Ver. 2.0

; SEQ ID NO 14  
; LENGTH: 289  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Fusion gene  
; OTHER INFORMATION: with homo sapien serine protease catalytic domain  
US-09-386-642-14

Query Match 43.6%; Score 598.5; DB 4; Length 289;  
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QY 21 KIFNGTEC-GRNSQPMQVGLFEGTSLRCGGVLDHRWLVTAACHGSGRYVRLGEHLSQ 79  
Db 51 KIVGYNCLPSPQWQAALFQGGQLCGVLGVGNVWLVTAACHCKPKYVRLGDHSLQN 110  
QY 80 LDWTEQIRHSGFVTHPGYLGAST-SHEHDLRLRLPLRVVTSSVQPLPLPNDCACTAGT 137  
Db 111 EECGEQTRTATESFPHPGFNNSLPNKDHNDIMLVKMASPVSIWAVRPLTSSRCVTAG 170  
QY 138 TECHVSGWGITNHPNPPDLPDLOCLNLSIVSHATCHGVYVPGRTITSNMVCAG-GVPGDAGC 196  
Db 171 TSLISGWTSSPQLRPLHLCANITIIHOKCENAYPGNITDTMVCASVGEKSDSC 230  
QY 197 QGDSGGLVCGGLVGLVSGVSGVPCQDGPVYVYICKYVDWIRMIMNN 248  
Db 231 QGDSGGLVNCQSLQIISWGQ-DPCAITRKPGVYVYICKYVDWIQETMKN 281

## RESULT 13

US-08-944-483-24  
; Sequence 24, Application US/08944483  
; Patent No. 6232456  
; GENERAL INFORMATION:  
; APPLICANT: COHEN, MAURICE  
; APPLICANT: COLPITTS, TRACEY L.  
; APPLICANT: FRIEDMAN, PAULA N.  
; APPLICANT: GRANADOS, EDWARD N.  
; APPLICANT: KLASS, MICHAEL R.  
; APPLICANT: RUSSELL, JOHN C.  
; APPLICANT: STEWART, KENT D.  
; APPLICANT: STROUPE, STEVEN D.  
; TITLE OF INVENTION: NOVEL SERINE PROTEASE REAGENTS  
; TITLE OF INVENTION: AND METHODS USEFUL FOR DETECTING AND TREATING DISEASES  
; TITLE OF INVENTION: OF THE PROSTATE  
; NUMBER OF SEQUENCES: 76  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Abbott Laboratories  
; STREET: 100 Abbott Park Road  
; CITY: Abbott Park  
; STATE: IL  
; COUNTRY: USA  
; ZIP: 60064-3500  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/944,483  
; FILING DATE:  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Becker, Cheryl L.  
; REGISTRATION NUMBER: 35,441  
; REFERENCE/DOCKET NUMBER: 6183.US.01  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 847/935-1729  
; TELEFAX: 847/938-2623



Qy 239 DWIRMINR 246  
||| :|  
Db 269 LWIRETIR 276

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Job time : 52 secs

GenCore version 5.1.6  
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Perfect score: 1374

Sequence: 1 MGSLIFLLCVLGLSQATP.....GVYTYICKYVDWIRMRNN 248

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Post-processing: Minimum Match 0%

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Listing first 1500 summaries

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Published Applications AA:\*

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- 7: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.pep.\*
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- 12: /cgn2\_6/ptodata/2/pubpaa/US09\_NEW\_PUB.pep.\*
- 13: /cgn2\_6/ptodata/2/pubpaa/US10A\_PUBCOMB.pep.\*
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- 19: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep.\*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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69	811	59.0	162	14	US-10-325-745-6
70	630.5	45.9	260	9	US-09-796-294-7
121	630.5	45.9	260	14	US-10-167-749-395
246	630.5	45.9	260	14	US-10-223-085-72
250	630.5	45.9	260	14	US-10-223-084-72
251	630.5	45.9	260	14	US-10-223-088-72
252	630.5	45.9	260	14	US-10-223-090-72
253	630.5	45.9	260	14	US-10-223-087-72
255	630.5	45.9	260	14	US-10-223-083-72
256	630.5	45.9	260	14	US-10-223-089-72
426	630.5	45.9	260	14	US-10-223-081-72

446	630.5	45.9	260	14	US-10-223-082-72	Sequence 72, Appl
472	630.5	45.9	260	14	US-10-461-787-7	Sequence 7, Appl
516	630.5	45.9	260	15	US-10-170-481A-395	Sequence 395, App
518	630.5	45.9	260	15	US-10-210-028-395	Sequence 395, App
577	630.5	45.9	260	15	US-10-162-521A-395	Sequence 395, App
585	630.5	45.9	260	15	US-10-305-654-72	Sequence 72, Appl
586	630.5	45.9	260	15	US-10-295-027-500	Sequence 500, App
588	630.5	45.9	260	15	US-10-173-999-125	Sequence 125, App
595	630.5	45.9	260	15	US-10-072-012-612	Sequence 612, App
598	630.5	45.9	260	15	US-10-262-511-62	Sequence 62, Appl
602	630.5	45.9	260	15	US-10-081-056-72	Sequence 72, Appl
603	630.5	45.9	260	15	US-10-344-394-32	Sequence 32, Appl
608	630.5	45.9	260	17	US-10-918-851-395	Sequence 395, App
609	630.5	45.9	260	17	US-10-931-886-396	Sequence 396, App
610	630.5	45.9	260	17	US-10-805-667-395	Sequence 395, App
611	630.5	45.9	260	17	US-10-897-359-395	Sequence 395, App
612	627	45.6	305	14	US-10-050-882-52	Sequence 52, Appl
613	627	45.6	315	15	US-10-264-049-2464	Sequence 2464, Ap
614	622.5	45.3	260	9	US-09-796-294-8	Sequence 8, Appl
615	622.5	45.3	260	9	US-09-968-415-7	Sequence 7, Appl
616	622.5	45.3	260	14	US-10-180-719-7	Sequence 8, Appl
617	622.5	45.3	260	14	US-10-461-787-8	Sequence 7, Appl
618	622.5	45.3	260	15	US-10-072-012-609	Sequence 609, App
619	621.5	45.2	260	15	US-10-072-012-610	Sequence 610, App
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651	618.5	45.0	250	14	US-10-004-860-427	Sequence 427, App
799	618.5	45.0	250	14	US-10-023-282-427	Sequence 427, App
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855	618.5	45.0	250	14	US-10-223-084-208	Sequence 208, App
856	618.5	45.0	250	14	US-10-223-088-208	Sequence 208, App
857	618.5	45.0	250	14	US-10-223-090-208	Sequence 208, App
862	618.5	45.0	250	14	US-10-205-823-212	Sequence 212, App
863	618.5	45.0	250	14	US-10-223-087-208	Sequence 208, App
870	618.5	45.0	250	14	US-10-223-083-208	Sequence 208, App
874	618.5	45.0	250	14	US-10-223-089-208	Sequence 208, App
1043	618.5	45.0	250	14	US-10-013-909A-170	Sequence 170, App
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1092	618.5	45.0	250	14	US-10-223-082-208	Sequence 208, App
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1216	618.5	45.0	250	15	US-10-295-027-560	Sequence 560, App
1217	618.5	45.0	250	15	US-10-173-999-160	Sequence 160, App
1224	618.5	45.0	250	15	US-10-055-569A-66	Sequence 66, Appl
1231	618.5	45.0	250	15	US-10-081-056-208	Sequence 208, App
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1241	618.5	45.0	282	15	US-10-055-569A-65	Sequence 65, Appl
1242	602.5	43.9	277	15	US-10-344-394-28	Sequence 28, Appl
1243	602.5	43.9	288	17	US-10-015-989A-13	Sequence 13, Appl
1244	601.5	43.8	250	11	US-09-978-360A-657	Sequence 657, App
1245	599.5	43.6	320	9	US-09-888-615-90	Sequence 90, Appl
1246	599.5	43.6	320	15	US-10-374-639-3	Sequence 3, Appl
1247	599.5	43.6	320	15	US-10-333-574-3	Sequence 3, Appl
1248	599	43.6	225	15	US-10-072-012-611	Sequence 611, App
1249	599	43.6	256	15	US-10-344-394-6	Sequence 6, Appl
1250	598.5	43.6	289	17	US-10-015-989A-14	Sequence 14, Appl
1251	597.5	43.5	248	11	US-09-789-210-24	Sequence 24, Appl
1252	597.5	43.5	249	15	US-10-055-569A-68	Sequence 68, Appl
1253	597.5	43.5	276	15	US-10-055-569A-67	Sequence 67, Appl
1254	593.5	43.2	260	15	US-10-072-012-613	Sequence 613, App
1255	573	41.7	247	15	US-10-651-790-4	Sequence 4, Appl
1256	569.5	41.4	251	15	US-10-344-394-27	Sequence 27, Appl
1257	568.5	41.4	250	15	US-10-055-569A-69	Sequence 69, Appl
1258	568.5	41.4	250	15	US-10-344-394-29	Sequence 29, Appl
1259	567	41.3	248	10	US-09-842-758-54	Sequence 54, Appl
1260	567	41.3	248	15	US-10-174-333-54	Sequence 54, Appl
1261	567	41.3	277	15	US-10-243-552-563	Sequence 563, App
1262	567	41.3	277	15	US-10-344-394-26	Sequence 26, Appl
1263	567	41.3	277	16	US-10-755-889-576	Sequence 576, App
1264	566.5	41.2	251	9	US-09-764-898-212	Sequence 212, App
1265	565	41.1	248	10	US-09-842-758-53	Sequence 53, Appl
1266	565	41.1	248	15	US-10-174-333-53	Sequence 53, Appl
1267	564.5	41.1	293	9	US-09-739-907-82	Sequence 82, Appl
1268	564.5	41.1	293	9	US-09-739-907-97	Sequence 97, Appl

1295 564.5 41.1 293 10 US-09-997-428-309  
1340 564.5 41.1 293 11 US-09-938-671-82  
1341 564.5 41.1 293 11 US-09-938-671-97

Sequence 309, App  
Sequence 82, Appl  
Sequence 97, Appl

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

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Run on: March 5, 2005, 17:48:47 ; Search time 40 seconds  
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596.544 Million cell updates/sec

Title: US-10-006-856A-194  
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Gapop 10.0 , Gapext 0.5

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Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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3: pir3.\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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6	555	40.4	253	2	A53968
7	553	40.2	246	2	B25528
8	552	40.2	229	1	TRBQTR
9	550	40.0	247	2	SI3813
10	546	39.7	247	1	TRDG
11	545	39.7	246	1	TRDGC
12	544.5	39.6	247	2	A27547
13	543	39.5	246	1	TRRT1
14	540	39.3	238	2	S31779
15	533.5	38.8	247	2	S05434
16	532	38.7	246	1	TRRT2
17	527.5	38.4	261	2	A31136
18	524	38.1	232	1	KQPG
19	520.5	37.9	261	2	A25606
20	519	37.8	246	2	QJ1471
21	518	37.7	245	2	QJ1472
22	518	37.7	261	2	A34079
23	513.5	37.4	239	2	S31778
24	513.5	37.4	239	2	A27207
25	511.5	37.2	261	2	S45303
26	510.5	37.2	261	1	NGMSG
27	508	37.0	242	2	S31776
28	508	37.0	242	2	S31775
29	503	36.6	260	2	A37938
30	503	36.6	263	2	S15686
31	502	36.5	259	2	B31136
32	501	36.5	247	1	B25852
33	498.5	36.4	241	2	S39048
34	496.5	36.1	261	1	TRMSMS
35	496	36.1	242	2	S49489
36	495.5	36.1	257	2	S33772
37	495.5	36.1	261	2	S01971
38	494.5	36.0	247	1	A25852
39	493	35.9	262	1	KQHU
40	491.5	35.8	240	2	S39047
41	491	35.7	256	1	NGMSA
42	490.5	35.7	229	1	TRDFS
43	490.5	35.7	261	2	A41020
44	489	35.6	244	2	A44284
45	485.5	35.3	261	2	JE0236
46	484.5	35.3	259	2	A29746
47	484.5	35.3	304	2	S33496
48	483.5	35.2	265	1	KQRTF
49	481.5	35.0	250	2	T01779
50	481.5	35.0	261	2	A29745
51	479	34.9	261	1	S35711
52	477.5	34.8	261	1	KQMS1
53	476	34.6	259	2	I38363
54	470.5	34.2	261	1	A32297
55	469.5	34.2	261	2	A24378
56	468	34.1	259	1	KQRTTN
57	467.5	34.0	261	1	EGMSB
58	467	34.0	247	2	SI2764
59	461.5	33.6	259	2	D23863
60	458.5	33.4	250	2	S31384
61	458.5	33.4	261	2	A29586
62	449	32.7	258	2	A57290
63	436.5	31.8	250	2	SI5685
64	436.5	31.8	257	1	JC2479
65	432	31.4	236	1	A32121
66	431.5	31.4	261	2	A28062
67	431	31.4	262	1	JG4803
68	422.5	30.7	233	1	JG0169
69	417	30.3	236	1	B3121
70	411.5	29.9	228	1	S35689
71	408	29.7	235	1	S65621
72	406.5	29.6	231	2	A60468
73	402	29.3	255	1	A28169
74	394	28.7	236	1	A41456
75	388	28.2	269	2	A26823
76	386	28.1	232	1	A54361
77	385.5	28.1	188	2	B32340
78	385.5	28.1	264	2	I38136
79	382.5	27.8	1524	2	T30337
80	382	27.8	246	1	DBHU
81	381	27.7	263	1	I55508
82	377	27.4	225	2	S45356
83	374.5	27.3	259	1	WMMS28
84	371	27.0	271	1	ELRT2
85	370.5	27.0	263	2	A21195
86	370	26.9	234	1	S20407
87	368.5	26.8	343	1	A57014
88	367.5	26.7	638	1	KQHUP
89	366	26.6	258	1	S36783
90	364	26.5	156	2	B23863
91	362.5	26.4	246	2	S64707
92	359.5	26.2	277	2	S35340
93	359	26.1	443	2	I46932
94	358	26.1	812	1	PLBO
95	357	26.0	262	1	A31372
96	357	26.0	273	2	A31299
97	357	26.0	271	2	S29239
98	357	26.0	1019	2	A38738
99	355.5	25.9	276	2	A38654
100	354	25.8	271	2	A25528
101	353.5	25.7	263	2	S47537
102	353.5	25.7	270	2	S56160

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venom B (EC 3.4  
snake venom factor  
gamma-amin (EC 3  
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mast cell proteina  
pancreatic elastas  
chymotrypsin (EC 3  
mast cell tryptase

103	353	25.7	274	2	JC4171	tryptase (EC 3.4.2	176	320.5	23.3	247	1	PRMSCL	granzyme B (EC 3.4
104	352	25.6	260	2	A45061	granzyme A (EC 3.4	177	319.5	23.3	559	1	A29941	t-plasminogen acti
105	352	25.6	461	1	JK0210	protein C activat	178	319.5	23.2	1034	1	A53663	entoropeptidase (E
106	351	25.5	456	1	KXBO	protein C activat	179	318.5	23.2	460	2	B61545	plasmin (EC 3.4.21
107	349.5	25.4	269	2	B26823	pancreatic elastas	180	318	23.1	265	2	T10495	chymotrypsin (EC 3
108	348	25.3	267	2	S40006	trypsin (EC 3.4.21	181	318	23.1	271	2	I46580	factor IX - pig (f
109	347	25.3	461	1	KXHU	protein C activat	182	318	23.1	274	2	I47078	coagulation factor
110	346.5	25.2	244	2	S26042	chymase (EC 3.4.21	183	318	23.1	618	2	A35827	thrombin (EC 3.4.2
111	346.5	25.2	461	1	S18994	protein C activat	184	317.5	23.1	245	1	KYBOB	chymotrypsin (EC 3
112	344	25.0	275	2	B35863	trypsin (EC 3.4.2	185	317.5	23.1	246	2	A32692	cytotoxic T-lympho
113	343.5	25.0	273	2	A47246	trypsin (EC 3.4.2	186	317	23.1	249	2	A55634	granzyme M (EC 3.4
114	343.5	25.0	274	2	S35339	trypsin (EC 3.4.21	187	316.5	23.0	246	1	A46504	chymase (EC 3.4.21
115	343	25.0	275	2	A32410	trypsin (EC 3.4.21	188	315.5	23.0	254	1	TRWV3Y	trypsin-like prote
116	342.5	24.9	558	2	JC5878	plasma hyaluronan-	189	315.5	23.0	266	1	ELRT1	pancreatic elastas
117	342.5	24.9	810	1	PLHU	trypsin (EC 3.4.21	190	315.5	23.0	392	1	A30100	serine proteinase
118	342	24.9	275	2	C35863	trypsin (EC 3.4.2	191	315.5	23.0	492	1	EXBO	coagulation factor
119	342	24.9	275	2	A35863	trypsin (EC 3.4.2	192	315	22.9	248	2	S43259	granzyme-like prot
120	341.5	24.9	258	2	I56220	trypsin 2 - rat	193	315	22.9	617	2	S10511	thrombin (EC 3.4.2
121	340.5	24.8	246	2	B38678	mast cell proteina	194	315	22.9	686	1	A59271	Ra-reactive factor
122	339.5	24.7	258	2	A45161	serine proteinase	195	314	22.9	275	2	S40005	trypsin (EC 3.4.21
123	339.5	24.7	267	4	A56615	probable pancreati	196	313	22.8	613	2	S15468	complement C3b/C4b
124	339	24.7	257	2	B45061	granzyme A (EC 3.4	197	313	22.8	855	2	JC7731	membrane-bound arg
125	339	24.7	461	1	KFHU	coagulation factor	198	312.5	22.7	274	2	S40004	trypsin-related pr
126	338	24.6	625	1	KFHU1	coagulation factor	199	312.5	22.7	615	1	KFHU12	coagulation factor
127	338	24.6	625	1	TBBO	thrombin (EC 3.4.2	200	311.5	22.7	761	2	JC5759	brain-specific ser
128	337.5	24.6	238	1	TRWV5Y	trypsin-like prote	201	311	22.6	261	2	S40162	cathepsin G (EC 3.
129	337.5	24.6	264	2	S65663	granzyme 3 (EC 3.4	202	311	22.6	431	2	S47538	u-plasminogen acti
130	337	24.5	434	1	A35005	u-plasminogen acti	203	311	22.6	433	1	JN0560	enteropeptidase (E
131	337	24.5	812	1	PLMS	plasmin (EC 3.4.21	204	311	22.6	1035	1	A43090	mast cell proteina
132	336.5	24.5	251	2	T10262	mast cell serine p	205	310.5	22.6	247	1	PRRTG	t-plasminogen acti
133	336.5	24.5	251	2	PC1235	29K serine protein	206	310.5	22.6	559	1	A35029	factor IX - rabbit
134	336.5	24.5	638	1	KPMSPL	plasma kallikrein	207	310	22.6	275	2	I46712	coagulation factor
135	336	24.5	416	1	KPBO	coagulation factor	208	309.5	22.5	482	1	EXRT	serine proteinase
136	336	24.5	790	1	PLPG	plasmin (EC 3.4.21	209	307	22.3	250	2	S55493	chymotrypsin (EC 3
137	335.5	24.4	258	4	S70439	pancreatic elastas	210	307	22.3	259	1	S49129	hepsin (EC 3.4.21.
138	333	24.2	245	1	KYBOA	chymotrypsin (EC 3	211	307	22.3	417	1	S00845	limulus clotting e
139	333	24.2	285	2	I48144	coagulation factor	212	306.5	22.3	375	1	A23689	thrombin (EC 3.4.2
140	332.5	24.2	638	1	KQRTPL	plasma kallikrein	213	305.5	22.2	236	2	I42696	granzyme B (EC 3.4
141	332.5	24.2	810	2	I46260	plasmin (EC 3.4.21	214	305	22.2	281	1	A61021	tissue kallikrein
142	332.5	24.2	810	2	B30848	trypsin (EC 3.4.21	215	304	22.1	149	1	KQMSM	thrombin (EC 3.4.2
143	331.5	24.1	256	1	TRFF	trypsin-like prote	216	304	22.1	268	2	C42696	pancreatic elastas
144	331.5	24.1	275	2	S40007	trypsin (EC 3.4.21	217	304	22.1	268	2	S68825	t-plasminogen acti
145	331	24.1	263	1	KYRTB	chymotrypsin (EC 3	218	304	22.1	562	1	UKHUT	chymase (EC 3.4.21
146	331	24.1	622	1	TBHU	thrombin (EC 3.4.2	219	303.5	22.1	244	2	A46721	coagulation factor
147	330.5	24.1	247	1	KXUOM	chymase (EC 3.4.21	220	303.5	22.1	309	2	B49878	hypothetical prote
148	330.5	24.1	560	1	JC4795	plasma hyaluronan-	221	303	22.1	196	2	T08808	mast cell proteina
149	330	24.0	282	2	I84631	coagulation factor	222	302.5	22.0	244	2	A34910	trypsin-related pr
150	330	24.0	4548	1	S00657	apoptein(a) (EC	223	302.5	22.0	273	2	S40003	oviductin (EC 3.4.
151	329.5	24.0	226	2	JB0151	myonase (EC 3.4.-	224	302.5	22.0	1004	2	T30338	low-density lipopr
152	329.5	24.0	237	2	S68702	trypsin (EC 3.4.2	225	302.5	22.0	1113	2	JE0315	pancreatic lipopr
153	329.5	24.0	269	2	C26823	pancreatic elastas	226	302	22.0	268	2	S68826	pancreatic elastas
154	329.5	24.0	1420	2	A32869	apolipoprotein(a)	227	302	22.0	394	2	JS0600	t-plasminogen acti
155	328.5	23.9	455	2	A61545	plasmin (EC 3.4.21	228	302	22.0	477	1	A34369	t-plasminogen acti
156	328.5	23.9	786	1	A47547	serine proteinase	229	302	22.0	477	2	JS0598	t-plasminogen acti
157	328	23.9	452	1	A30351	coagulation factor	230	301	21.9	255	2	A27122	cathepsin G (EC 3.
158	327.5	23.8	266	2	S54146	trypsin (EC 3.4.21	231	301	21.9	431	2	JS0599	u-plasminogen acti
159	327	23.8	244	2	S72219	chymotrypsin B - A	232	300.5	21.9	442	1	UKPG	kallikrein-like se
160	327	23.8	259	2	S68424	allergen Der f III	233	300	21.8	245	2	A48598	thrombin (EC 3.4.2
161	326.5	23.8	248	1	PRMSCL	granzyme C (EC 3.4	234	299.5	21.8	245	2	E42896	mast cell proteina
162	326.5	23.8	266	1	ELPG	pancreatic elastas	235	299.5	21.8	246	2	A38678	chymotrypsin (EC 3
163	326	23.7	248	2	S33755	granzyme-like prot	236	299.5	21.8	258	1	S44184	acrosin (EC 3.4.21
164	324	23.6	274	2	A45754	trypsin (EC 3.4.2	237	299.5	21.8	436	2	JS0172	acrosin (EC 3.4.21
165	324	23.6	459	2	JQ0419	coagulation factor	238	299	21.8	437	2	S18407	complement factor
166	324	23.6	1019	1	A56318	enteropeptidase (E	239	298.5	21.7	191	2	S54115	chymase (EC 3.4.21
167	323.5	23.5	466	1	KFHU7	coagulation factor	240	298.5	21.7	249	1	A35842	pancreatic elastas
168	322	23.4	699	1	I54763	Ra-reactive factor	241	298.5	21.7	270	2	B29934	coagulation factor
169	321.5	23.4	251	2	JC2125	chymase (EC 3.4.21	242	298.5	21.7	407	1	KFC07	trypsin (EC 3.4.21
170	321	23.4	226	1	KCTF	bradykinin (EC 3.4	243	297	21.6	237	1	TRCV1	trypsin (EC 3.4.21
171	321	23.4	226	2	S69370	duodenase - bovine	244	297	21.6	260	2	S26043	chymase (EC 3.4.21
172	321	23.4	247	2	S64708	chymase (EC 3.4.21	245	297	21.6	418	2	A37344	acrosin (EC 3.4.21
173	321	23.4	248	2	A43520	natural killer cel	246	297	21.6	477	2	JS0597	t-plasminogen acti
174	321	23.4	269	2	B32410	mastocytoma protei	247	296.5	21.6	248	1	S01007	granzyme F (EC 3.4
175	321	23.4	655	1	A46688	hepatocyte growth	248	296	21.5	281	2	T13596	trypsin homolog -

249	295.5	21.5	239	2	G42696	thrombin (EC 3.4.2	322	220.5	16.0	267	1	ELHUL	leukocyte elastase
250	295.5	21.5	433	1	UKMS	u-plasminogen acti	323	217.5	15.8	710	1	I51283	hepatocyte growth
251	294	21.4	247	2	S23504	chymase (EC 3.4.21	324	216	15.7	728	1	A35644	hepatocyte growth
252	294	21.4	303	2	T13598	trypsin homolog -	325	216	15.7	728	1	A60185	hepatocyte growth
253	293.5	21.4	431	1	UKHU	u-plasminogen acti	326	204.5	14.9	177	2	S23505	chymase (EC 3.4.21
254	293	21.3	234	2	F42696	thrombin (EC 3.4.2	327	201	14.6	214	2	S17680	fibrolytic prote
255	293	21.3	247	2	S59135	mast cell proteinase	328	197.5	14.4	213	2	S17537	chymotrypsin (EC 3
256	293	21.3	265	2	A38894	serine proteinase	329	196	14.3	248	2	S49323	complement factor
257	293	21.3	265	2	J50260	serine proteinase	330	192.5	14.0	763	2	I50807	tissue kallikrein
258	293	21.3	433	1	UKBAY	u-plasminogen acti	331	189.5	13.8	94	2	PC2013	tissue kallikrein
259	292.5	21.3	236	2	A28566	T-cell suppressor	332	182	13.2	104	2	S15395	haptoglobin - rhes
260	291.5	21.2	271	1	KVH20	chymotrypsin (EC 3	333	180	13.1	258	2	G02959	serine proteinase
261	291	21.2	261	2	S41308	serine proteinase	334	179.5	13.1	149	2	S35208	haptoglobin-relate
262	289.5	21.1	248	2	A34112	cytotoxic T-lympho	335	178	13.0	348	1	HPHUR	haptoglobin precu
263	289	21.0	583	2	A29154	complement factor	336	177	12.9	347	1	HPHUI	haptoglobin precu
264	288.5	21.0	270	2	A29934	pancreatic elastas	337	177	12.9	406	1	HPHU2	haptoglobin precu
265	288.5	21.0	1047	2	A56173	masquerade precurs	338	176.5	12.8	760	1	C2MS	classical-compleme
266	288	21.0	268	2	J01473	pancreatic elastas	339	176	12.8	735	2	T35778	probable fusidic a
267	288	21.0	421	2	S29599	acrosin (EC 3.4.21	340	174.5	12.7	377	2	C88710	protein C43G2.5 (i
268	287.5	20.9	235	2	H42696	thrombin (EC 3.4.2	341	174	12.7	161	2	I48158	coagulation factor
269	287.5	20.9	603	2	S28941	coagulation factor	342	174	12.7	330	2	B82415	probable serine pr
270	286.5	20.9	218	1	KVH2C	chymotrypsin (EC 3	343	172	12.5	346	2	I36942	haptoglobin - chim
271	286	20.8	254	2	S35585	chymotrypsin-like	344	171	12.4	159	2	S35202	proteinase 2 - buf
272	285.5	20.6	331	2	T27906	hypothetical prote	345	171	12.4	258	2	I36945	haptoglobin Hp - c
273	285	20.6	332	2	T27906	hypothetical prote	346	171	12.4	345	2	I36941	haptoglobin - chim
274	282	20.5	416	1	S33777	hepsin (EC 3.4.21	347	170	12.4	347	2	G00006	haptoglobin - blac
275	280	20.4	254	2	S65465	trypsin-like prote	348	169	12.3	329	1	HPDG	haptoglobin precu
276	278.5	20.3	593	2	S45281	coagulation factor	349	168	12.2	66	2	I52972	kallikrein - mouse
277	277.5	20.2	266	2	JC4850	trypsin-like prote	350	168	12.2	154	2	S35207	proteinase 7 - buf
278	276	20.1	430	1	A24702	serine proteinase	351	166	12.1	258	2	I36947	haptoglobin Hpp -
279	276	20.1	488	1	EXHU	coagulation factor	352	166	12.1	349	2	I36944	haptoglobin - chim
280	275.5	20.1	240	1	CPBOA3	procarboxypeptidas	353	166	12.1	752	1	C2HU	complement C2 prec
281	275	20.0	237	2	S55378	serine proteinase	354	165	12.0	161	2	I62744	coagulation factor
282	274.5	20.0	695	1	S05008	complement subcomp	355	165	12.0	347	1	HPMS	haptoglobin precu
283	273	19.9	247	2	S45113	granzyme-like prot	356	159.5	11.6	152	2	S35209	serine proteinase
284	273	19.9	265	2	T15451	hypothetical prote	357	159	11.6	126	2	A23473	chymotrypsin-like
285	272.5	19.8	432	1	S18932	u-plasminogen acti	358	158.5	11.5	264	2	A28942	pancreatic elastas
286	272	19.8	475	1	EXCH	coagulation factor	359	157.5	11.5	764	1	BBHU	complement factor
287	272	19.8	688	1	CIHUS	complement subcomp	360	154.5	11.2	747	2	I51579	complement factor
288	271	19.7	2616	2	A57096	ndel protein prec	361	153.5	11.2	761	1	BBMS	complement factor
289	270	19.7	694	2	JC6554	complement subcomp	362	152.5	11.1	159	2	I84615	coagulation factor
290	269.5	19.6	248	2	S33756	granzyme-like prot	363	152	11.1	181	2	T08805	hypothetical prote
291	269	19.6	256	1	PRHU3	proteinase 3 (EC 3	364	151.5	11.0	152	2	S35203	serine proteinase
292	268.5	19.5	420	2	A55283	acrosin (EC 3.4.21	365	148	10.8	81	2	A18966	tissue kallikrein
293	265	19.3	415	1	A34170	acrosin (EC 3.4.21	366	145.5	10.6	82	2	T46510	hypothetical prote
294	264.5	19.3	256	2	T10109	trypsin (EC 3.4.21	367	138.5	10.1	158	2	S35201	serine proteinase
295	264.5	19.3	264	2	S27994	trypsin-like prote	368	138	10.0	153	2	S35204	proteinase 4 - buf
296	263.5	19.2	251	1	TRHUA2	azurocidin precurs	369	137	10.0	743	2	T34853	probable fusidic a
297	261.5	19.0	366	2	J80105	testicular serine	370	136.5	9.9	152	2	S35206	serine proteinase
298	261.5	19.0	421	1	S11674	acrosin (EC 3.4.21	371	135.5	9.9	46	2	I49416	glandular kallikre
299	259	18.9	248	2	S01006	cytotoxic T-lympho	372	132	9.6	347	1	HPRT	haptoglobin precu
300	258.5	18.8	252	2	A36172	procytotoxic T-lym	373	129.5	9.4	396	1	KXBOZ	plasma protein 2 -
301	258.5	18.8	285	2	T35195	probable serine pr	374	127.5	9.3	69	2	S28195	tissue kallikrein
302	257.5	18.7	254	2	S49329	trypsin-like prote	375	127.5	9.3	72	2	S28196	tissue kallikrein
303	256	18.6	400	2	C82228	probable trypsin V	376	126	9.2	80	2	A05324	gamma-amin (EC 3
304	252	18.3	400	1	A48050	coagulation factor	377	123.5	9.0	137	2	S55364	serine proteinase
305	248	18.0	367	2	J50104	testicular serine	378	123.5	9.0	151	2	S35205	proteinase 5 - buf
306	247	18.0	243	2	A56338	venom proteinase (	379	122.5	8.9	75	2	A37002	catrobin I (EC 3
307	245	17.8	711	1	A47136	macrophage-stimula	380	115.5	8.4	422	1	KXHU2	plasma protein 2 p
308	244.5	17.8	716	1	A40332	macrophage-stimula	381	114.5	8.3	85	2	S44461	elastase (EC 3.4.2
309	239.5	17.4	265	2	I48679	neutrophil elastas	382	109.5	8.0	61	2	PS0049	serine proteinase
310	237.5	17.3	232	2	S23398	serine proteinase	383	108	7.9	333	2	T15257	hypothetical prote
311	235.5	17.1	198	2	S06176	cytotoxic T-lympho	384	104.5	7.6	256	2	A56593	trypsin-related pr
312	235.5	17.1	716	1	JC5061	macrophage-stimula	385	104	7.6	49	2	B24696	tissue kallikrein
313	235	17.1	96	2	A05308	tissue kallikrein	386	103.5	7.5	64	2	A30981	prostatic arginine
314	235	17.1	230	2	A27802	hypodermin C (EC 3	387	99.5	7.2	340	2	T34423	hypothetical prote
315	234.5	17.1	219	1	TRPGA2	azurocidin - pig	388	97	7.1	388	2	A34672	alkaline serine pr
316	233	17.0	705	1	CIHURB	complement subcomp	389	96.5	7.0	416	2	AH2387	hypothetical prote
317	231.5	16.8	230	2	I48685	mast cell proteina	390	94.5	6.9	416	2	G71965	glycine hydroxymet
318	227.5	16.6	272	2	JC4170	trypsin-like prote	391	93.5	6.8	73	2	S44462	elastase (EC 3.4.2
319	227	16.5	259	1	TRSMG	trypsin (EC 3.4.21	392	93.5	6.8	299	1	PRSMBG	streptogrisin B (E
320	226	16.4	728	1	JH0579	hepatocyte growth	393	92.5	6.7	416	2	G64542	glycine hydroxymet
321	225	16.4	548	2	D82175	probable trypsin V	394	91	6.6	31	2	A18671	tissue kallikrein



541	74	5.4	886	2	150694	collagen alpha 1(I	614	71.5	5.2	895	2	T49010	hypothetical prote
542	74	5.4	1124	1	I58388	protein-tyrosine k	615	71.5	5.2	918	2	JC4361	scavenger receptor
543	74	5.4	1413	2	T26467	hypothetical prote	616	71	5.2	181	2	S56532	hypothetical 20K p
544	74	5.4	1670	1	CGH03B	collagen alpha 3(I	617	71	5.2	316	2	S25264	viik protein - Shi
545	74	5.4	1677	2	T14267	Xin protein, stage	618	71	5.2	359	2	E70806	probable regulator
546	73.5	5.3	246	2	T16403	hypothetical prote	619	71	5.2	407	2	AI0595	imidazolonepropion
547	73.5	5.3	294	2	T29838	hypothetical prote	620	71	5.2	458	2	T31631	hypothetical prote
548	73.5	5.3	305	2	B84413	hypothetical prote	621	71	5.2	490	2	T37884	transcription fact
549	73.5	5.3	321	2	T28760	hypothetical prote	622	71	5.2	497	2	B42827	interleukin enhanc
550	73.5	5.3	346	2	JA0159	cysteine proteinas	623	71	5.2	575	2	A97635	adenine deaminase
551	73.5	5.3	411	2	A65184	arylsulfatase acti	624	71	5.2	575	2	AC2858	hypothetical glyci
552	73.5	5.3	482	2	AE0839	succinate-semialde	625	71	5.2	639	2	D70931	hypothetical prote
553	73.5	5.3	483	2	D83613	succinate-semialde	626	71	5.2	818	2	B75606	hypothetical prote
554	73.5	5.3	525	1	S38794	cellulose 1,4-beta	627	71	5.2	883	2	T51221	hypothetical prote
555	73.5	5.3	680	1	CGHUID	collagen alpha 1(X	628	71	5.2	1230	2	E64664	outer membrane pro
556	73.5	5.3	724	2	A48569	antigen Em100 - Ei	629	71	5.2	1391	2	T20406	hypothetical prote
557	73.5	5.3	791	2	D64629	iron-regulated out	630	71	5.2	1691	1	S22917	collagen alpha 5(I
558	73.5	5.3	1806	1	CGHUIE	collagen alpha 1(X	631	71	5.2	1717	1	A45558	epidermal growth f
559	73	5.3	50	2	S55674	cerastocytin (EC 3	632	71	5.2	2164	1	GNVY89	genome polypeptin
560	73	5.3	295	2	T22833	hypothetical prote	633	71	5.2	2531	2	S18188	notch protein homo
561	73	5.3	360	2	T36763	probable secreted	634	71	5.2	2531	2	T16743	hypothetical prote
562	73	5.3	508	2	B70865	probable transmemb	635	71	5.2	3512	2	T17121	CPV protein - midg
563	73	5.3	597	2	S71352	metalloproteinase	636	70.5	5.1	238	2	S28001	omotin-like prote
564	73	5.3	662	2	I38400	melanoma-associate	637	70.5	5.1	284	2	T29528	hypothetical prote
565	73	5.3	707	1	TSBYAB	tryptophan synthas	638	70.5	5.1	290	2	AE1176	fructokinases homo
566	73	5.3	728	2	S43768	transcription acti	639	70.5	5.1	325	2	T06784	GTP-binding protei
567	73	5.3	767	2	T05662	hypothetical prote	640	70.5	5.1	325	2	T09613	probable GTP-bindi
568	73	5.3	881	2	S25445	nitrate reductase	641	70.5	5.1	339	2	T22607	hypothetical prote
569	73	5.3	997	2	A60776	230k bullous pemph	642	70.5	5.1	356	2	S66348	cysteine proteinas
570	73	5.3	1339	2	JC4387	epidermal growth f	643	70.5	5.1	366	2	S11449	collagen short cha
571	73	5.3	1744	2	S40991	collagen alpha 1(I	644	70.5	5.1	396	1	TRYXB4	alpha-lytic protei
572	73	5.3	2207	1	GNVY5P	genome polypeptin	645	70.5	5.1	400	2	T35106	probable secreted
573	73	5.3	2555	2	A40043	notch protein homo	646	70.5	5.1	423	2	A41207	collagen 13, nonfi
574	73	5.3	3061	1	JN0545	genome polypeptin	647	70.5	5.1	585	2	T37526	probable transcrip
575	73	5.3	3623	2	T08618	intrinsic factor-B	648	70.5	5.1	627	2	T35608	polyketide hydroxy
576	72.5	5.3	155	1	T12M1	trypsin/factor XII	649	70.5	5.1	630	2	T43460	hypothetical prote
577	72.5	5.3	230	2	D85553	probable chaperone	650	70.5	5.1	860	1	EAMS	elastin precursor
578	72.5	5.3	230	2	A90703	probable chaperone	651	70.5	5.1	920	2	A45748	collagen alpha 1(V
579	72.5	5.3	230	2	B64785	molecular chaperon	652	70.5	5.1	1342	2	A36223	kinase-related tra
580	72.5	5.3	286	2	C81681	dihydrodipicolinat	653	70.5	5.1	1414	1	S23809	collagen alpha 2(I
581	72.5	5.3	302	2	T32872	hypothetical prote	654	70.5	5.1	1466	1	B40333	collagen alpha 1(I
582	72.5	5.3	328	2	JC5350	2-nitrotoluene red	655	70.5	5.1	1747	2	A54121	collagen alpha 4 c
583	72.5	5.3	362	2	T35287	probable secreted	656	70.5	5.1	3198	2	A43426	collagen alpha 2 f
584	72.5	5.3	488	2	T47697	Regulator of chrom	657	70	5.1	261	2	S40210	chlorophyll a/b-bi
585	72.5	5.3	606	2	T08180	P20 protein, micr	658	70	5.1	283	2	JS0170	collagen col-19 -
586	72.5	5.3	1132	2	T03844	telomerase catalyt	659	70	5.1	285	2	S60598	hypothetical prote
587	72.5	5.3	1497	2	I49607	procollagen type V	660	70	5.1	300	2	T19929	hypothetical prote
588	72.5	5.3	1514	2	T34869	glutamate synthase	661	70	5.1	304	2	T26185	hypothetical prote
589	72	5.2	207	2	T46415	hypothetical prote	662	70	5.1	304	2	T26184	hypothetical prote
590	72	5.2	220	2	T18553	probable O-methylt	663	70	5.1	313	2	T26465	hypothetical prote
591	72	5.2	229	2	D95358	hypothetical prote	664	70	5.1	315	2	C95941	probable transcrip
592	72	5.2	258	2	A29259	Ubx protein - fru1	665	70	5.1	343	2	JQ2170	hemagglutinin - in
593	72	5.2	392	2	A56123	streptogrisin D (E	666	70	5.1	389	2	I49263	potential oncogene
594	72	5.2	577	2	B37057	integrin beta-6 ch	667	70	5.1	389	2	A59392	Wnt10b protein pre
595	72	5.2	673	2	F89101	protein F25E5.7 [i	668	70	5.1	395	1	T45547	arylsulfatase acti
596	72	5.2	691	2	T44543	probable bacteriop	669	70	5.1	402	2	H82228	imidazolonepropion
597	72	5.2	814	2	T49207	receptor kinase-li	670	70	5.1	485	2	F97228	glu-TRNAGln amidot
598	72	5.2	957	2	T15976	hypothetical prote	671	70	5.1	548	2	H82432	sucrose-6-phosphat
599	72	5.2	1220	2	A56136	jagged protein pre	672	70	5.1	560	2	D84205	hypothetical prote
600	72	5.2	2150	1	GNVYH2	genome polypeptin	673	70	5.1	561	2	C75343	6-aminohexanoate-c
601	72	5.2	2194	1	GNVY87	genome polypeptin	674	70	5.1	671	1	CGRT1S	collagen alpha 1(I
602	72	5.2	2205	1	GNVY26	genome polypeptin	675	70	5.1	674	2	S23297	collagen alpha 1(X
603	71.5	5.2	58	2	A45526	collagen homolog A	676	70	5.1	798	2	T28906	hypothetical prote
604	71.5	5.2	236	2	T24799	hypothetical prote	677	70	5.1	863	2	A53034	gag polypeptin -
605	71.5	5.2	283	2	JC5579	chymotrypsin-like	678	70	5.1	877	2	S49197	envelope protein p
606	71.5	5.2	284	2	T27032	probable thiosulfa	679	70	5.1	938	2	C84480	hypothetical prote
607	71.5	5.2	297	2	T18638	hypothetical prote	680	70	5.1	1188	2	D86236	protein F14N23.5 [
608	71.5	5.2	305	2	T20906	hypothetical prote	681	70	5.1	1366	2	T35985	probable large pro
609	71.5	5.2	466	2	I39707	probable indoleace	682	70	5.1	2043	2	T18524	scavenger receptor
610	71.5	5.2	524	2	T04623	cruciferin F2009.2	683	70	5.1	2206	1	GNVY4P	genome polypeptin
611	71.5	5.2	547	2	T29717	hypothetical prote	684	70	5.1	2206	1	GNVY27	genome polypeptin
612	71.5	5.2	665	1	VMVKA	env polypeptin pr	685	70	5.1	2206	2	S03822	genome polypeptin
613	71.5	5.2	793	2	ARH2126	hypothetical prote	686	70	5.1	4391	2	A38096	perlecan precursor

687	69.5	5.1	126	2	S47010	Ig heavy chain V4.	760	68.5	5.0	337	2	H86582	CT 368 hypothetical
688	69.5	5.1	184	2	E82345	probable galactosyl	761	68.5	5.0	357	2	H89819	conserved hypothet
689	69.5	5.1	244	1	LNM5MC	mannose-binding le	762	68.5	5.0	372	2	S60207	fomF protein - Str
690	69.5	5.1	248	1	LNDGFS	pulmonary surfacta	763	68.5	5.0	412	2	G86003	probable transport
691	69.5	5.1	250	2	S30157	osmotin precursor	764	68.5	5.0	412	2	A91158	protein transport
692	69.5	5.1	275	2	A84179	endonuclease IV [i	765	68.5	5.0	412	2	B65134	cysteine proteinas
693	69.5	5.1	303	2	T19289	hypothetical prote	766	68.5	5.0	427	2	S57776	MFS pernease limpo
694	69.5	5.1	337	2	T23794	hypothetical prote	767	68.5	5.0	487	2	AP2692	hypothetical prote
695	69.5	5.1	353	2	S16785	hemagglutinin - in	768	68.5	5.0	528	2	B97474	spore coat protein
696	69.5	5.1	356	2	S16907	collagen alpha 1(I	769	68.5	5.0	537	2	B33485	conserved hypothet
697	69.5	5.1	382	2	S20375	collagen alpha 3(V	770	68.5	5.0	544	2	G87330	collagen alpha cha
698	69.5	5.1	432	2	F96919	ABC transporter (p	771	68.5	5.0	547	2	A36046	4-alpha-D-((1->4) -
699	69.5	5.1	466	2	T06416	cysteine proteinas	772	68.5	5.0	575	2	JC7727	MPL-K protein prec
700	69.5	5.1	482	2	S76475	hypothetical prote	773	68.5	5.0	579	2	B45266	nitrous-oxide redu
701	69.5	5.1	545	2	C82617	NH3-dependent NAD	774	68.5	5.0	634	1	S24384	MPL-P protein prec
702	69.5	5.1	656	2	JC2005	integrin beta-5 ch	775	68.5	5.0	635	2	A45266	collagen alpha 1(I
703	69.5	5.1	739	2	C87559	phosphoribosylform	776	68.5	5.0	673	1	CGBO6C	collagen alpha 1(X
704	69.5	5.1	749	2	I38488	prothinin - huma	777	68.5	5.0	674	2	S13301	probable membrane-
705	69.5	5.1	1024	2	S18251	collagen alpha 1(X	778	68.5	5.0	677	2	F95910	collagen alpha 1(V
706	69.5	5.1	1181	2	C97851	DNA-directed DNA p	779	68.5	5.0	744	1	A34246	collagen alpha 1(V
707	69.5	5.1	1418	2	T45467	collagen alpha 1(I	780	68.5	5.0	744	1	S23298	collagen alpha 1(V
708	69.5	5.1	1464	2	S59856	collagen alpha 1(I	781	68.5	5.0	744	2	S15435	collagen alpha 1(X
709	69.5	5.1	1487	1	CGHU6C	collagen alpha 1(X	782	68.5	5.0	888	2	S28791	hypothetical prote
710	69.5	5.1	1603	2	S23810	probable polyketid	784	68.5	5.0	915	2	T21772	hypothetical prote
711	69.5	5.1	1986	2	S28353	tenascin precursor	785	68.5	5.0	927	2	I53282	gene PACB4 protein
712	69.5	5.1	2019	1	JQ1322	tenascin precursor	786	68.5	5.0	937	2	I53282	collagen alpha 1(I
713	69.5	5.1	2201	2	A32160	pseudo-kallikrein	787	68.5	5.0	1049	1	CG807S	collagen alpha 1(I
714	69.5	5.0	38	2	T01677	finger protein (cl	788	68.5	5.0	1419	2	A41182	collagen alpha 1(I
715	69.5	5.0	224	2	S06545	mannose-binding le	789	68.5	5.0	2206	1	GNNY21	genome polyprotein
716	69.5	5.0	239	1	LNM5MA	hypothetical prote	790	68.5	5.0	2403	2	A59386	sanko - human
717	69.5	5.0	290	2	T24586	hypothetical prote	791	68.5	5.0	2482	2	I48922	cation-independent
718	69.5	5.0	290	2	T24590	hypothetical prote	792	68.5	5.0	2483	1	A49617	insulin-like growt
719	69.5	5.0	294	2	T21668	hypothetical glyci	793	68.5	5.0	2560	1	I40457	peptide synthetase
720	69.5	5.0	297	1	PRSMAG	streptogrisin A (E	794	68.5	5.0	2715	2	T13049	eyelid - fruit fly
721	69.5	5.0	327	2	S48839	guanine nucleotide	795	68.5	5.0	3106	1	S53868	laminin alpha-2 ch
722	69.5	5.0	329	2	B83162	molybdopterin bios	796	68.5	5.0	4544	1	S02392	alpha-2-macroglobu
723	69.5	5.0	334	1	S74957	cytochrome c-type	797	68.5	5.0	4660	2	T42737	gp330 protein prec
724	69.5	5.0	395	2	S41035	hypothetical prote	798	68.5	5.0	4660	2	A60010	early EIA 20K prot
725	69.5	5.0	399	2	H84717	hypothetical prote	799	68.5	5.0	1775	2	S37749	collagen alpha 2(X
726	69.5	5.0	406	2	A47696	acetamidase - Myco	799	68.5	5.0	1777	2	S37749	nitrite hydratase
727	69.5	5.0	435	2	T39719	beta transducin -	800	68.5	5.0	229	1	S54799	protein C3H4.4 [i
728	69.5	5.0	438	2	T50991	hypothetical prote	801	68.5	5.0	237	2	A88640	mannose-binding le
729	69.5	5.0	441	2	A45565	cysteine proteinas	802	68.5	5.0	248	1	LNHUMC	probable conserved
730	69.5	5.0	469	2	A24450	collagen alpha 2(V	803	68.5	5.0	272	2	H87075	hypothetical prote
731	69.5	5.0	533	2	B95922	hypothetical nucle	804	68.5	5.0	289	2	T27708	nicotinate-nucleot
732	69.5	5.0	532	2	F70560	hypothetical glyci	805	68.5	5.0	297	2	T46864	hypothetical prote
733	69.5	5.0	567	1	C55516	hydrogenase (EC 1.	806	68.5	5.0	330	2	T26004	hemagglutinin HAI
734	69.5	5.0	567	2	G85958	probable large sub	807	68.5	5.0	343	1	HMIVTA	G2R protein - vari
735	69.5	5.0	567	2	G91113	hydrogenase-2 larg	808	68.5	5.0	349	2	D72175	hemagglutinin - in
736	69.5	5.0	613	2	T11464	NADH2 dehydrogenas	809	68.5	5.0	354	2	A35788	hemagglutinin - in
737	69.5	5.0	635	2	A57131	collagen alpha 2(V	810	68.5	5.0	358	2	T26281	hypothetical prote
738	69.5	5.0	682	2	D84579	probable Tail-like	811	68.5	5.0	384	2	S46110	hypothetical prote
739	69.5	5.0	950	2	S27473	URBS1 protein - sm	812	68.5	5.0	387	2	B49175	Notch A protein -
740	69.5	5.0	1366	1	CGHU2S	collagen alpha 2(I	813	68.5	5.0	404	2	A54871	Gal beta-1, 3GalNA
741	69.5	5.0	1669	1	CGHU4B	collagen alpha 1(I	814	68.5	5.0	412	2	JC6317	glutamate dehydrog
742	69.5	5.0	1749	2	S75071	hypothetical prote	815	68.5	5.0	447	2	F82862	conjugat transfer
743	69.5	5.0	1786	1	MMHUB1	laminin beta-1 cha	816	68.5	5.0	453	2	S49168	beta tubulin 1 - r
744	69.5	5.0	2207	2	S09553	genome polypotein	817	68.5	5.0	460	2	A93938	phosphotransferase
745	69.5	5.0	2209	1	GNNY2P	genome polypotein	818	68.5	5.0	484	2	F98208	succinate-semialde
746	69.5	5.0	2450	2	S71625	protein-tyrosine-p	819	68.5	5.0	484	2	AC3078	aldehyde denydroge
747	69.5	5.0	4957	2	T03455	ALR protein - huma	820	68.5	5.0	490	2	E95316	succinate-semialde
748	69.5	5.0	5262	2	T03454	ALR protein - huma	821	68.5	5.0	543	2	A41285	interleukin enhanc
749	68.5	5.0	127	2	F82617	ferredoxin XF1964	822	68.5	5.0	566	1	HMIV	hemagglutinin prec
750	68.5	5.0	155	2	B32669	vasotocin 2 / neur	823	68.5	5.0	566	1	HMIV17	hemagglutinin prec
751	68.5	5.0	233	2	S31829	pathogenesis-relat	824	68.5	5.0	605	2	TM5291	sphingomyelin phos
752	68.5	5.0	250	2	S25114	osmotin-like prote	825	68.5	5.0	631	2	JC2345	kexin-like protein
753	68.5	5.0	252	2	A55047	collagen alpha 1(V	826	68.5	5.0	656	2	G85731	Rhs element associ
754	68.5	5.0	285	2	T18814	hypothetical prote	827	68.5	5.0	680	2	S31216	collagen alpha 1(X
755	68.5	5.0	290	2	AI1533	fructokinases homo	828	68.5	5.0	724	2	T27858	probable peroxidase
756	68.5	5.0	323	2	T19142	hypothetical prote	829	68.5	5.0	726	2	T35865	probable cyclase -
757	68.5	5.0	329	2	T32783	hypothetical prote	830	68.5	5.0	743	1	S23779	collagen alpha 1(V
758	68.5	5.0	336	1	S76928	probable aryl alco	831	68.5	5.0	754	2	A55267	collagen alpha 5(I
759	68.5	5.0	337	2	A72042	conserved hypothet	832	68.5	5.0	756	2	S67433	hypothetical prote

833	68	4.9	759	2	B70585	hypothetical prote	906	67	4.9	651	2	A26581	beta-glucuronidase
834	68	4.9	864	2	A48266	protein-tyrosine k	907	67	4.9	653	2	G96675	hypothetical prote
835	68	4.9	972	2	A30363	glycoprotein GP130	908	67	4.9	686	2	JC7569	Delta-4 protein -
836	68	4.9	1223	2	T17345	hypothetical prote	909	67	4.9	737	2	S65758	nitrate reductase
837	68	4.9	1331	2	S05011	calcium channel al	910	67	4.9	756	2	AH1022	arginine decarboxy
838	68	4.9	1400	2	E90886	RNase core protein	911	67	4.9	884	2	T18649	hypothetical prote
839	68	4.9	1493	2	A44224	DNA repair helicase	912	67	4.9	919	2	T16150	hypothetical prote
840	68	4.9	1786	1	MMMSB1	laminin beta-1 cha	913	67	4.9	1012	2	T13603	probable N-methyl-
841	68	4.9	2100	2	T03223	probable polyketid	914	67	4.9	1027	2	S28774	collagen alpha cha
842	68	4.9	2209	1	GNNX3P	genome polyprotein	915	67	4.9	1034	2	JC5598	mucin - rat
843	68	4.9	2767	1	UIHU	thyroglobulin prec	916	67	4.9	1051	2	A35763	collagen alpha 2 c
844	67.5	4.9	73	1	HPRB	hypoglobulin precu	917	67	4.9	1084	2	A40136	fibropellin la - s
845	67.5	4.9	242	1	AE1868	hypothetical prote	918	67	4.9	1136	2	DNBEHF	DNA-binding protei
846	67.5	4.9	287	1	LNRBPS	pulmonary surfacta	919	67	4.9	1196	1	DNBEV1	major DNA-binding
847	67.5	4.9	246	2	S34665	collagen, cuticula	920	67	4.9	1373	1	A43291	collagen alpha 2(I
848	67.5	4.9	296	2	T21070	hypothetical prote	921	67	4.9	1466	1	CGHU7L	collagen alpha 1(I
849	67.5	4.9	307	2	T16842	hypothetical prote	922	67	4.9	1632	2	C70752	probable ctpi prot
850	67.5	4.9	315	2	T34332	hypothetical prote	923	67	4.9	1705	2	S51672	adenylate cyclase
851	67.5	4.9	315	2	AE2384	hypothetical prote	924	67	4.9	1747	2	A45974	collagen alpha 1(X
852	67.5	4.9	325	2	S02170	hypothetical prote	925	67	4.9	1761	2	T13990	collagen type IV a
853	67.5	4.9	330	2	S46657	collagen alpha 1(I	926	67	4.9	1775	2	A31893	collagen alpha 1(I
854	67.5	4.9	337	2	A83026	collagen alpha 1(X	927	67	4.9	1857	2	S31212	collagen alpha 1(X
855	67.5	4.9	339	2	E82211	conserved hypotet	928	67	4.9	1888	2	S78476	collagen alpha 1(X
856	67.5	4.9	336	2	A25918	thrombomodulin - b	929	67	4.9	2269	1	JQ1750	genome polyprotein
857	67.5	4.9	369	2	T02150	probable (S)-2-hyd	930	67	4.9	2524	2	A35844	Xotch protein - Af
858	67.5	4.9	383	2	T31771	hypothetical prote	931	67	4.9	3282	2	E82750	hemagglutinin-like
859	67.5	4.9	399	2	C95943	probable choline u	932	66.5	4.8	35	2	I49403	complement factor
860	67.5	4.9	412	2	AB1000	type II secretion	933	66.5	4.8	119	2	S41111	pancreatic ribonuc
861	67.5	4.9	411	2	S61562	hypothetical prote	934	66.5	4.8	122	2	JL0047	ig heavy chain v r
862	67.5	4.9	528	2	T10622	hypothetical prote	935	66.5	4.8	140	2	A49045	ig heavy chain v r
863	67.5	4.9	627	2	V0888	hypothetical prote	936	66.5	4.8	140	2	T21857	hypothetical prote
864	67.5	4.9	665	1	VCMVVR	env polyprotein pr	937	66.5	4.8	243	2	S34794	osmotin - common t
865	67.5	4.9	674	2	T19268	hypothetical prote	938	66.5	4.8	244	1	LNRTMC	mannose-binding le
866	67.5	4.9	771	2	S35681	ESG protein - mous	939	66.5	4.8	251	2	H75495	hypothetical prote
867	67.5	4.9	846	1	PNECA	penicillin amidase	940	66.5	4.8	278	2	H87663	hypothetical prote
868	67.5	4.9	850	2	S56015	Gastric mucin MUC5	941	66.5	4.8	294	2	G72706	hypothetical prote
869	67.5	4.9	861	2	A48825	Notch homolog Muc	942	66.5	4.8	301	2	T23441	hypothetical prote
870	67.5	4.9	977	2	I52657	seizure-related pr	943	66.5	4.8	303	2	E90444	conserved hypotet
871	67.5	4.9	1010	2	T36383	probable large ATP	944	66.5	4.8	304	2	T22482	hypothetical prote
872	67.5	4.9	1091	1	PL0009	complement C3d/Eps	945	66.5	4.8	316	2	T19291	hypothetical prote
873	67.5	4.9	1208	2	T27822	hypothetical prote	946	66.5	4.8	337	2	S55932	NCA3 protein precu
874	67.5	4.9	1242	1	DJBSC1	DNA-directed DNA p	947	66.5	4.8	345	2	AH0350	probable DNA-bindi
875	67.5	4.9	1373	2	JE0095	Gastric mucin MUC5	948	66.5	4.8	377	2	JC7535	chitinase (EC 3.2.
876	67.5	4.9	1574	2	T13954	MEGF6 protein - ra	949	66.5	4.8	388	2	JC6164	circumsporozoite p
877	67.5	4.9	1706	1	OYBRC	cyclolysin - Borde	950	66.5	4.8	417	2	T08724	hypothetical prote
878	67.5	4.9	1810	1	A32230	tenascin precursor	951	66.5	4.8	428	2	T19309	hypothetical prote
879	67.5	4.9	1838	1	CGHU1V	collagen alpha 1(V	952	66.5	4.8	506	2	F83547	sodium/proline sym
880	67.5	4.9	1843	2	S18803	collagen alpha 1(V	953	66.5	4.8	560	2	H70466	serine proteinase
881	67.5	4.9	2531	2	T31070	notch-1 protein - se	954	66.5	4.8	576	2	T38293	hypothetical serin
882	67.5	4.9	2531	2	A46019	notch-1 protein -	955	66.5	4.8	589	2	S66856	probable membrane
883	67.5	4.9	6642	2	T29757	protein UNC-89 - C	956	66.5	4.8	589	2	S50355	alpha-glucosidase
884	67	4.9	133	2	H84217	hypothetical prote	957	66.5	4.8	598	2	S65770	maltoligosyltreha
885	67	4.9	163	1	A34313	antifreeze protein	958	66.5	4.8	660	2	S71949	metallopeptidase
886	67	4.9	171	1	JBA041	chorion class B pr	959	66.5	4.8	673	2	A48089	growth arrest-spec
887	67	4.9	183	2	P01009	keratin-like prote	960	66.5	4.8	675	2	S20819	collagen alpha 3(I
888	67	4.9	239	2	S07406	thauartin homolog	961	66.5	4.8	685	2	JC7570	Delta-4 protein -
889	67	4.9	253	2	S49158	complement protein	962	66.5	4.8	688	2	E86409	hypothetical prote
890	67	4.9	264	2	S73040	hypothetical prote	963	66.5	4.8	742	2	JC7595	scavenger receptor
891	67	4.9	272	2	S57460	cytochrome-c oxida	964	66.5	4.8	751	2	S64741	cuticle collagen -
892	67	4.9	299	2	A47031	biaphos acetylhy	965	66.5	4.8	828	2	G82583	bifunctional aspar
893	67	4.9	327	2	T32164	hypothetical prote	966	66.5	4.8	1085	2	T18369	K-Cl cotransport p
894	67	4.9	336	2	H81091	probable CDP-6-deo	967	66.5	4.8	1085	2	T31429	K-Cl cotransport p
895	67	4.9	343	2	JQ2372	hemagglutinin - in	968	66.5	4.8	1086	2	T14114	K-Cl cotransport p
896	67	4.9	343	2	JQ2371	hemagglutinin - in	969	66.5	4.8	1091	2	A58532	glial cell membran
897	67	4.9	344	2	PQ0321	hemagglutinin - in	970	66.5	4.8	1225	1	OYURCP	spect receptor p
898	67	4.9	344	2	JQ1643	hemagglutinin - in	971	66.5	4.8	2318	2	S45306	notch 3 protein -
899	67	4.9	378	2	E75621	probable chromosom	972	66.5	4.8	2471	2	A49128	cell-fate determin
900	67	4.9	401	2	A73341	precorrin-6y c5,15	973	66.5	4.8	2703	1	A24420	notch protein - fr
901	67	4.9	404	2	T44281	iron-sulfur cofact	974	66.5	4.8	2769	1	UIBO	thyroglobulin prec
902	67	4.9	427	2	T20800	hypothetical prote	975	66.5	4.8	2944	2	A54849	collagen alpha 1(V
903	67	4.9	456	2	D84651	hypothetical prote	976	66.5	4.8	3707	2	S18252	heparan sulfate pr
904	67	4.9	466	2	C42360	cellulase (EC 3.2.	977	66	4.8	98	2	AG1960	hypothetical prote
905	67	4.9	566	1	HMIYD1	hemagglutinin prec	978	66	4.8	170	2	AC0689	alternative bacter

979	66	4.8	238	1	LNRTMA	mannose-binding le	1052	65.5	4.8	1629	2	C84839	ferredoxin-depende
980	66	4.8	239	2	D82727	6-phosphogluconola	1053	65.5	4.8	2518	2	A12140	polyketide synthas
981	66	4.8	256	2	AE0997	probable biotin bi	1054	65.5	4.8	2823	2	F87908	protein T22A3.8 fi
982	66	4.8	306	2	T21938	hypothetical prote	1055	65.5	4.8	2823	2	T23064	hypothetical prote
983	66	4.8	307	2	T18846	hypothetical prote	1056	65.5	4.8	3102	2	T43291	laminin alpha chai
984	66	4.8	311	2	S48400	carrier protein FL	1057	65.5	4.8	3871	2	T22812	hypothetical prote
985	66	4.8	313	2	A35122	metalloproteinase	1058	65.5	4.8	4848	2	T30289	pristinamycin I sy
986	66	4.8	326	2	JQ1437	hemagglutinin - in	1059	65	4.7	111	2	B82830	hypothetical prote
987	66	4.8	336	2	S41643	syrm protein - Rhi	1060	65	4.7	162	2	T43957	ribosomal protein
988	66	4.8	336	2	AE0997	hemagglutinin - in	1061	65	4.7	181	2	T07661	maturation protein
989	66	4.8	344	2	PQ0319	hypothetical prote	1062	65	4.7	188	2	A54270	insulin-like growt
990	66	4.8	348	2	T29288	hypothetical prote	1063	65	4.7	188	2	B54270	insulin-like growt
991	66	4.8	353	2	D96596	hypothetical prote	1064	65	4.7	229	1	S19713	nitrite hydratase
992	66	4.8	355	1	S37460	glutaryl endopepti	1065	65	4.7	232	2	E70789	probable protease -
993	66	4.8	435	2	T15143	hypothetical prote	1066	65	4.7	249	2	F70925	hypothetical prote
994	66	4.8	553	2	T23362	hypothetical prote	1067	65	4.7	287	2	D70625	probable transposa
995	66	4.8	614	2	T06741	hypothetical prote	1068	65	4.7	299	2	T20605	hypothetical prote
996	66	4.8	687	2	T02459	probable beta-amyl	1069	65	4.7	303	2	S45461	hypothetical prote
997	66	4.8	753	2	S35371	finger protein neu	1070	65	4.7	311	2	F75366	hypothetical prote
998	66	4.8	787	2	T05617	hypothetical prote	1071	65	4.7	313	2	H89865	hypothetical prote
999	66	4.8	854	2	A96574	protein F12M16.30	1072	65	4.7	342	2	A46396	ets-related protei
1000	66	4.8	864	2	T30441	probable capsid-as	1073	65	4.7	349	2	T43457	hypothetical prote
1001	66	4.8	1194	2	C09436	KIAA1391 protein l	1074	65	4.7	356	2	T22827	hypothetical prote
1002	66	4.8	1964	2	T09059	notch4 - mouse	1075	65	4.7	358	2	T36415	probable iron-side
1003	66	4.8	2113	2	E96505	hypothetical prote	1076	65	4.7	416	2	H82968	probable fumarylac
1004	66	4.8	2193	2	S52319	polyprotein (IA, 1	1077	65	4.7	428	2	D83861	hypothetical prote
1005	66	4.8	3442	2	E82589	hemagglutinin-like	1078	65	4.7	446	2	T10711	anthranilate N-ben
1006	66	4.8	3455	2	B82519	hemagglutinin-like	1079	65	4.7	469	2	T36362	probable DNA repl
1007	65.5	4.8	3507	2	T34513	hypothetical prote	1080	65	4.7	476	2	T29054	probable transmem
1008	65.5	4.8	37	2	S03570	trypsin (EC 3.4.21	1081	65	4.7	619	2	T08613	hypothetical prote
1009	65.5	4.8	97	2	JH0428	ig heavy chain V r	1082	65	4.7	711	2	D86296	glycine hydroxymet
1010	65.5	4.8	114	2	I72667	ig gamma chain V r	1083	65	4.7	715	2	S52675	sarcosine oxidase
1011	65.5	4.8	117	2	T35913	cold agglutinin FS	1084	65	4.7	737	2	T02178	probable fumarylac
1012	65.5	4.8	140	2	S78052	ig heavy chain pre	1085	65	4.7	759	2	T44142	hypothetical prote
1013	65.5	4.8	147	2	A84546	SOS ribosomal prot	1086	65	4.7	784	2	JQ0317	probable serine-th
1014	65.5	4.8	202	2	T35703	hypothetical prote	1087	65	4.7	826	2	A60385	hypothetical glyci
1015	65.5	4.8	208	2	T49891	glycine-rich prote	1088	65	4.7	837	2	E70835	CotC protein precu
1016	65.5	4.8	245	1	C1HUQA	complement subcomp	1089	65	4.7	866	2	S57936	hypothetical prote
1017	65.5	4.8	286	2	F71524	dihydrodipicolinat	1090	65	4.7	881	2	T49279	hypothetical prote
1018	65.5	4.8	298	2	T27644	hypothetical prote	1091	65	4.7	984	2	T00326	hypothetical prote
1019	65.5	4.8	304	2	JC5845	chitinase (EC 3.2.	1092	65	4.7	1112	2	S49432	replicase 126K - o
1020	65.5	4.8	311	2	E85867	hypothetical prote	1093	65	4.7	1196	1	DNBEKS	DNA-binding protei
1021	65.5	4.8	311	2	D91023	hypothetical prote	1094	65	4.7	1374	2	T16129	hypothetical prote
1022	65.5	4.8	327	2	AG3367	alcohol dehydrogen	1095	65	4.7	1374	2	T02087	gag/pol polyprotei
1023	65.5	4.8	350	2	S63248	hypothetical prote	1096	65	4.7	1439	2	D70807	hypothetical glyci
1024	65.5	4.8	360	2	T37285	collagen dpv-2 - C	1097	65	4.7	1489	2	T00028	brain-specific ang
1025	65.5	4.8	363	2	T16831	hypothetical prote	1098	65	4.7	1522	2	T00028	3-dehydroquinatase
1026	65.5	4.8	371	2	B72461	hypothetical prote	1099	65	4.7	1603	1	BVASA1	collagen alpha 2(I
1027	65.5	4.8	396	2	T29773	hypothetical prote	1100	65	4.7	1707	2	A33526	hypothetical glyci
1028	65.5	4.8	397	2	S28274	collagen alpha 2(I	1101	65	4.7	1901	2	F70806	CRP-ductin-alpha p
1029	65.5	4.8	402	1	CG8028	hypothetical prote	1102	65	4.7	2083	2	T42721	calcium channel pr
1030	65.5	4.8	452	2	T30082	gene 61 protein -	1103	65	4.7	2166	2	S11339	calcium channel al
1031	65.5	4.8	467	1	WZBE61	cytochrome b558/56	1104	65	4.7	2171	2	S05054	RNA-directed RNA p
1032	65.5	4.8	479	2	C90457	collagen alpha 1(I	1105	65	4.7	2244	2	T08212	protein-tyrosine-p
1033	65.5	4.8	488	2	T23735	catalase (EC 1.11.	1106	65	4.7	2294	2	T08212	surface protein ty
1034	65.5	4.8	576	2	S33327	collagen alpha 1(I	1107	65	4.7	2395	1	S50820	protein-tyrosine-p
1035	65.5	4.8	615	2	A05269	collagen alpha 1(I	1108	65	4.7	2466	2	I67629	protein-tyrosine-p
1036	65.5	4.8	691	2	A54741	erythrocyte membra	1109	65	4.7	2490	1	A54971	fatty-acid synthas
1037	65.5	4.8	730	2	A36226	collagen alpha 1 c	1110	65	4.7	2509	2	G01880	gamma-P-crystallin
1038	65.5	4.8	741	2	G69514	hypothetical prote	1111	65	4.7	159	2	I49618	collagen alpha 1(I
1039	65.5	4.8	775	2	A61228	collagen alpha 2(I	1112	65	4.7	171	2	A34493	lipote biosynthes
1040	65.5	4.8	782	2	B83966	formate dehydrogen	1113	65	4.7	191	2	D90712	lipote biosynthes
1041	65.5	4.8	877	2	T03098	p97 protein - Toxo	1114	65	4.7	191	2	D64797	lipote biosynthes
1042	65.5	4.8	947	2	T23107	hypothetical prote	1115	65	4.7	210	2	T20973	hypothetical prote
1043	65.5	4.8	966	1	P1BVB8	RNA Ia protein - b	1116	65	4.7	222	2	A88102	protein W09G10.1 l
1044	65.5	4.8	969	2	B87083	exonuclease ABC s	1117	64.5	4.7	232	2	E90834	minor tail protein
1045	65.5	4.8	1137	2	T02097	glutamate synthase	1118	64.5	4.7				
1046	65.5	4.8	1210	1	GOHUE	epidermal growth f	1119	64.5	4.7				
1047	65.5	4.8	1295	2	A32901	glp1 protein precu	1120	64.5	4.7				
1048	65.5	4.8	1353	1	JQ2168	E2 glycoprotein pr	1121	64.5	4.7				
1049	65.5	4.8	1360	2	T33942	hypothetical prote	1122	64.5	4.7				
1050	65.5	4.8	1376	1	JQ1534	E2 glycoprotein pr	1123	64.5	4.7				
1051	65.5	4.8	1492	2	A40333	collagen alpha 1'	1124	64.5	4.7				



1125	64.5	4.7	242	2	560143	cellulase (EC 3.2.	1198	64	4.7	426	2	D88103	protein W10G11.6 [
1126	64.5	4.7	262	2	A54889	IgE-binding protei	1199	64	4.7	465	1	S47738	cytochrome-c perox
1127	64.5	4.7	266	2	T22706	hypothetical prote	1200	64	4.7	465	2	F91178	cytochrome-c perox
1128	64.5	4.7	277	1	Q0BEC2	HKRF protein - hu	1201	64	4.7	465	2	G86024	cytochrome-c perox
1129	64.5	4.7	297	2	T27525	hypothetical prote	1202	64	4.7	487	2	T45923	hypothetical prote
1130	64.5	4.7	301	2	B31219	collagen 2 - Caeno	1203	64	4.7	502	2	S35226	L1 protein - human
1131	64.5	4.7	317	2	T29960	hypothetical prote	1204	64	4.7	504	2	S56745	mucin (clone pGM31
1132	64.5	4.7	318	2	S27977	cuticle collagen d	1205	64	4.7	516	2	S42093	cellulose 1,4-beta
1133	64.5	4.7	328	2	AD1916	alcohol dehydrogen	1206	64	4.7	566	1	HMIVUR	hemagglutinin prec
1134	64.5	4.7	333	2	T15867	hypothetical prote	1207	64	4.7	566	2	S69888	hemagglutinin prec
1135	64.5	4.7	354	2	B75400	phosphoribosylform	1208	64	4.7	595	2	F95379	probable adenine d
1136	64.5	4.7	356	2	T05119	leucoanthocyanidin	1209	64	4.7	663	1	S18572	tetracycline resis
1137	64.5	4.7	387	2	E95933	probable calcium-b	1210	64	4.7	669	2	A35103	cell surface recep
1138	64.5	4.7	398	2	B71284	probable periplasm	1211	64	4.7	697	2	T37946	hypothetical prote
1139	64.5	4.7	411	2	B91220	probable arylsulfa	1212	64	4.7	717	2	T49238	hypothetical prote
1140	64.5	4.7	411	2	D86066	probable arylsulfa	1213	64	4.7	719	2	A87292	primosomal protein
1141	64.5	4.7	411	2	S58105	Cu metalloregulato	1214	64	4.7	721	2	F70649	probable Acyl-CoA
1142	64.5	4.7	416	2	T41665	probable dipeptida	1215	64	4.7	728	2	I50719	C-Delta-1 - chicke
1143	64.5	4.7	445	2	D86620	phosphoshikimate v	1216	64	4.7	753	2	AH0097	probable biotin su
1144	64.5	4.7	445	2	C72004	phosphoshikimate v	1217	64	4.7	823	2	T21104	hypothetical prote
1145	64.5	4.7	460	1	Q0RT	hemopexin precursor	1218	64	4.7	843	2	T13334	probable tail-host
1146	64.5	4.7	529	2	S36578	L1 protein - human	1219	64	4.7	861	2	B49847	nitrate reductase
1147	64.5	4.7	532	2	AE1964	Dnak-type molecula	1220	64	4.7	895	2	AD0541	outer membrane fim
1148	64.5	4.7	547	1	A32244	60K cysteine-rich	1221	64	4.7	963	2	T19140	hypothetical prote
1149	64.5	4.7	553	2	D71515	60K cysteine-rich	1222	64	4.7	998	2	T35745	probable ATP-bindi
1150	64.5	4.7	562	2	A85524	choline dehydrogen	1223	64	4.7	1000	2	AB3467	sarcosine oxidase
1151	64.5	4.7	562	2	E90673	choline dehydrogen	1224	64	4.7	1083	2	H86921	probable arabinosy
1152	64.5	4.7	570	2	S42708	proline transport	1225	64	4.7	1955	1	AGCH	agrin precursor -
1153	64.5	4.7	570	2	S04547	proline transport	1226	64	4.7	2042	2	T18399	variant-specific s
1154	64.5	4.7	597	2	JC7615	alpha-glucosidase	1227	64	4.7	2321	2	S78549	notch3 protein - h
1155	64.5	4.7	599	2	T25835	hypothetical prote	1228	64	4.7	3137	2	A37797	collagen alpha 3 (V
1156	64.5	4.7	618	2	S32436	collagen alpha 2(I	1229	64	4.7	3461	2	S58870	reelin precursor -
1157	64.5	4.7	626	2	C72035	succinate dehydrog	1230	64	4.7	3635	2	T10053	lamin alpha 5 ch
1158	64.5	4.7	626	2	C86589	succinate dehydrog	1231	64	4.7	7463	2	T36248	CDA peptide synthe
1159	64.5	4.7	644	2	JC2346	kexin-like protein	1232	63.5	4.6	97	2	G34564	Ig heavy chain V-I
1160	64.5	4.7	646	2	H96665	protein F22C12.10	1233	63.5	4.6	144	2	S24805	hypothetical prote
1161	64.5	4.7	653	1	S23667	cytochrome c-type	1234	63.5	4.6	152	2	T24064	hypothetical prote
1162	64.5	4.7	653	2	T02080	probable carbonat	1235	63.5	4.6	184	2	D83234	hypothetical prote
1163	64.5	4.7	666	2	F71310	probable periplasm	1236	63.5	4.6	191	2	I46412	keratin KAP5, 4 - s
1164	64.5	4.7	678	2	B84856	hypothetical prote	1237	63.5	4.6	191	2	AF0580	lipote-protein li
1165	64.5	4.7	715	2	S70397	zona pellucida gly	1238	63.5	4.6	215	2	AD0455	thiamine-phosphate
1166	64.5	4.7	721	2	C84732	probable homeodoma	1239	63.5	4.6	220	2	S35789	US2 protein - bovi
1167	64.5	4.7	724	2	C71274	hypothetical prote	1240	63.5	4.6	232	1	TLBPLL	minor tail protein
1168	64.5	4.7	730	2	H86295	hypothetical prote	1241	63.5	4.6	234	2	T31753	hypothetical prote
1169	64.5	4.7	884	2	S61569	hypothetical prote	1242	63.5	4.6	253	1	C1HUQB	complement subcomp
1170	64.5	4.7	1374	1	GNVVEC	ganome polypeptin	1243	63.5	4.6	256	2	T28853	hypothetical prote
1171	64.5	4.7	1376	1	VGIRJ2	E2 glycoprotein pr	1244	63.5	4.6	269	2	C83516	hypothetical prote
1172	64.5	4.7	1388	2	A53317	collagen alpha 1(X	1245	63.5	4.6	281	2	T32765	hypothetical prote
1173	64.5	4.7	1408	2	S16148	gene serrate, prote	1246	63.5	4.6	281	2	C88638	protein F58F6.1 [i
1174	64.5	4.7	1487	2	T02850	hypothetical prote	1247	63.5	4.6	289	2	T34241	hypothetical prote
1175	64.5	4.7	1546	1	CGHU2E	collagen alpha 2(X	1248	63.5	4.6	289	2	T26812	hypothetical prote
1176	64.5	4.7	1712	1	CGHU2B	collagen alpha 2(I	1249	63.5	4.6	290	2	A32249	collagen - sea urc
1177	64.5	4.7	2139	2	A35672	crumbs protein - f	1250	63.5	4.6	291	2	T34494	hypothetical prote
1178	64.5	4.7	3623	2	T09456	intrinsic factor-B	1251	63.5	4.6	294	2	T23916	hypothetical prote
1179	64	4.7	104	2	JH0345	T-cell receptor al	1252	63.5	4.6	308	2	H90452	conserved hypoteth
1180	64	4.7	118	1	A31429	hisactophilin [val	1253	63.5	4.6	311	2	B64998	hypothetical prote
1181	64	4.7	128	2	JQ1002	keratin, claw - ch	1254	63.5	4.6	316	2	T20497	hypothetical prote
1182	64	4.7	133	2	B38911	Ig heavy chain V r	1255	63.5	4.6	320	2	C81029	3-oxoacyl-(acyl-ca
1183	64	4.7	218	2	T03287	osmotin protein ho	1256	63.5	4.6	320	2	T39110	probable gpase ac
1184	64	4.7	238	2	B75266	phosphoribosylform	1257	63.5	4.6	326	2	T02340	GTP-binding regula
1185	64	4.7	248	1	LNHUP6	pulmonary surfacta	1258	63.5	4.6	328	2	T16970	GTP-binding protei
1186	64	4.7	278	2	C43670	integral membrane	1259	63.5	4.6	335	2	A40038	MHC class I histoc
1187	64	4.7	304	2	T23801	hypothetical prote	1260	63.5	4.6	338	2	T49182	probable chloropla
1188	64	4.7	310	2	T29731	hypothetical prote	1261	63.5	4.6	357	2	H75541	probable oxidoredu
1189	64	4.7	333	2	T50630	hypothetical prote	1262	63.5	4.6	371	2	B88633	protein F56B3.1 [i
1190	64	4.7	346	2	T45069	8-hydroxy-guanine	1263	63.5	4.6	375	2	A95867	probable pyroloquo
1191	64	4.7	394	1	VGEB17	glycoprotein D pre	1264	63.5	4.6	378	2	AB0894	conserved hypoteth
1192	64	4.7	394	1	VGEB17	glycoprotein D - h	1265	63.5	4.6	381	2	T27806	hypothetical prote
1193	64	4.7	401	2	C89102	protein F25E5.10 [	1266	63.5	4.6	388	2	T22553	hypothetical prote
1194	64	4.7	411	2	T16382	glutamate dehydrog	1267	63.5	4.6	404	2	T40553	Trp-asn repeat pro
1195	64	4.7	411	2	T04342	glutamate dehydrog	1268	63.5	4.6	418	2	S31124	hypothetical prote
1196	64	4.7	411	2	T03294	glutamate dehydrog	1269	63.5	4.6	435	2	B87412	conserved hypoteth
1197	64	4.7	426	2	AH2144	hypothetical prote	1270	63.5	4.6	445	2	C72695	probable amidase A

1271	63.5	4.6	481	2	A33712	metalloproteinase	1344	63	4.6	437	2	JC7138	alpha-amylase (EC
1272	63.5	4.6	498	2	B84789	probable protein w	1345	63	4.6	437	2	TJ0946	alpha-amylase 3E -
1273	63.5	4.6	504	1	P1WL31	I1 protein - human	1346	63	4.6	438	2	D89206	protein nhr-21, a I
1274	63.5	4.6	538	2	S65764	chitinase (EC 3.2.	1347	63	4.6	453	2	A71891	glu-tRNA amidotran
1275	63.5	4.6	556	1	S10901	choline dehydrogen	1348	63	4.6	453	2	AE2955	glutamyl-tRNA amid
1276	63.5	4.6	654	2	A34734	transcription fact	1349	63	4.6	471	2	A39024	collagen alpha 3(I
1277	63.5	4.6	660	2	C90343	conserved hypotet	1350	63	4.6	475	2	AE0855	conserved hypotet
1278	63.5	4.6	680	2	T25832	hypothetical prote	1351	63	4.6	475	2	H91077	probable 4-hydroxy
1279	63.5	4.6	690	2	T08504	hypothetical prote	1352	63	4.6	475	2	T44997	probable 4-hydroxy
1280	63.5	4.6	700	2	T41401	spore outgrowth fa	1353	63	4.6	475	2	A85923	probable 4-hydroxy
1281	63.5	4.6	724	2	D87530	isoquinoline 1-oxi	1354	63	4.6	480	2	T70785	hypothetical prote
1282	63.5	4.6	728	2	S26427	70K structural pro	1355	63	4.6	487	2	T21384	hypothetical prote
1283	63.5	4.6	742	4	C34734	transcription fact	1356	63	4.6	513	1	EUTQ1	cellulose 1,4-beta
1284	63.5	4.6	768	2	A42755	P-selectin precurs	1357	63	4.6	513	2	H82282	cellulose 1,4-beta
1285	63.5	4.6	803	2	C83561	probable type II s	1358	63	4.6	543	2	T03079	probable carbonat
1286	63.5	4.6	825	4	B34734	transcription fact	1359	63	4.6	545	2	S10099	transcription fact
1287	63.5	4.6	872	2	S49538	CoC protein precu	1360	63	4.6	582	2	T27013	hypothetical prote
1288	63.5	4.6	883	2	T07651	potassium channel	1361	63	4.6	611	2	T27155	hypothetical prote
1289	63.5	4.6	901	2	T04108	receptor kinase ho	1362	63	4.6	622	2	B40983	collagen alpha 1(X
1290	63.5	4.6	907	2	T15792	hypothetical prote	1363	63	4.6	638	2	I53169	cytokeatin 2 - hu
1291	63.5	4.6	932	2	I52527	PAC5A - mouse (fr	1364	63	4.6	638	2	AE1782	glucose inhibited
1292	63.5	4.6	1042	2	T26844	hypothetical prote	1365	63	4.6	658	2	AB3253	hypothetical prote
1293	63.5	4.6	1345	2	S46817	hypothetical prote	1366	63	4.6	684	2	F83375	translation elonga
1294	63.5	4.6	1381	2	E70806	hypothetical glyci	1367	63	4.6	692	2	C83666	translation elonga
1295	63.5	4.6	1549	2	I48103	type VII collagen	1368	63	4.6	692	2	T44380	translation elonga
1296	63.5	4.6	1573	2	S01845	DNA (cytosine-5)-	1369	63	4.6	695	2	AE1406	translation elonga
1297	63.5	4.6	1649	2	C86822	hypothetical prote	1370	63	4.6	695	2	AE1782	translation elonga
1298	63.5	4.6	1693	2	S76086	beta transducin-l1	1371	63	4.6	695	2	AE1782	nuclease, probable
1299	63.5	4.6	1959	1	AGRT	agrin - rat	1372	63	4.6	695	2	G87316	hypothetical prote
1300	63.5	4.6	2185	1	GNNYBT	genome polyprotein	1373	63	4.6	705	2	C84406	eye cell developme
1301	63.5	4.6	2185	1	JQ2021	genome polyprotein	1374	63	4.6	760	2	A45174	hypothetical prote
1302	63.5	4.6	2195	2	T34264	hypothetical prote	1375	63	4.6	946	2	T16297	hypothetical prote
1303	63.5	4.6	2322	2	T30201	Notch homolog prot	1376	63	4.6	1125	1	S57846	protein-tyrosine k
1304	63.5	4.6	2533	2	T28675	alpha-5ID-immobil	1377	63	4.6	1170	2	A53612	laminin Blk chain
1305	63.5	4.6	2533	2	T28674	fatty-acid synthas	1378	63	4.6	1203	2	A43175	Notch B protein -
1306	63.5	4.6	2533	2	S55505	hypothetical prote	1379	63	4.6	1331	2	T18310	receptor-adenylate
1307	63.5	4.6	3063	2	T13853	hypothetical prote	1380	63	4.6	1345	2	S55669	tegument protein 7
1308	63	4.6	3429	2	A49081	capillary permeabi	1381	63	4.6	1367	2	T33819	latent transformin
1309	63	4.6	99	2	S26801	Ig heavy chain v r	1382	63	4.6	1820	2	A55494	genome polyprotein
1310	63	4.6	119	2	B45937	early chorion prot	1383	63	4.6	2157	1	GNNY1B	transmembrane prot
1311	63	4.6	119	2	S24294	chorion protein -	1384	63	4.6	2437	2	S42612	gelation factor AB
1312	63	4.6	198	2	A31153	hypothetical prote	1385	63	4.6	2647	2	A37098	collagen alpha 3(V
1313	63	4.6	212	2	E86179	hypothetical prote	1386	63	4.6	3176	2	CGHUA3	Ig heavy chain V r
1314	63	4.6	228	2	A49882	collagen UCOLI - p	1387	62.5	4.5	97	2	S14474	phospholipase A2 (
1315	63	4.6	240	2	F70631	probable sodC prot	1388	62.5	4.5	118	2	S29653	textilotoxin chain
1316	63	4.6	242	1	F75433	probable phosphos	1389	62.5	4.5	144	2	S01391	insulin-like growt
1317	63	4.6	245	1	CIHUQC	complement subcomp	1390	62.5	4.5	155	2	C44012	hypothetical prote
1318	63	4.6	248	1	LNHUPS	pulmonary surfacta	1391	62.5	4.5	165	2	S72776	hypothetical prote
1319	63	4.6	257	2	T28946	hypothetical prote	1392	62.5	4.5	181	2	A70627	collagen alpha 1(I
1320	63	4.6	265	2	AG0814	cob(I)alamin adeno	1393	62.5	4.5	198	2	I49558	phosphoglycerate m
1321	63	4.6	289	2	S36166	paired box transcr	1394	62.5	4.5	214	2	T18539	glycine-rich prote
1322	63	4.6	285	2	T29982	hypothetical prote	1395	62.5	4.5	222	2	S19931	Ig Fab region IV-J
1323	63	4.6	299	2	T24833	hypothetical prote	1396	62.5	4.5	231	2	B23746	osmoitin-like prote
1324	63	4.6	302	2	T15936	hypothetical prote	1397	62.5	4.5	247	2	S33197	hypothetical prote
1325	63	4.6	303	2	E86591	CT580 hypothetical	1398	62.5	4.5	299	2	T29956	hypothetical prote
1326	63	4.6	303	2	D72031	neurosporene hydro	1399	62.5	4.5	306	2	H81036	riboflavin kinase/
1327	63	4.6	308	2	S32172	hypothetical prote	1400	62.5	4.5	313	2	T33010	hypothetical prote
1328	63	4.6	309	2	H69595	probable 3-oxoacyl	1401	62.5	4.5	316	2	T19288	hypothetical prote
1329	63	4.6	320	2	C81972	collagen col-14 -	1402	62.5	4.5	341	2	F70625	hypothetical prote
1330	63	4.6	326	2	JS0169	hypothetical prote	1403	62.5	4.5	352	2	JE0296	thyrotropin releas
1331	63	4.6	348	2	T28623	gene G4R endopepti	1404	62.5	4.5	356	2	S61061	hypothetical prote
1332	63	4.6	349	2	D36858	glutamyl endopepti	1405	62.5	4.5	359	2	T22774	hypothetical prote
1333	63	4.6	357	1	S33321	surfactant protein	1406	62.5	4.5	391	2	F87258	acyl-CoA dehydroge
1334	63	4.6	369	2	S33603	hypothetical prote	1407	62.5	4.5	398	2	AG0128	1-deoxy-D-xylulose
1335	63	4.6	383	2	A83518	serine proteinase,	1408	62.5	4.5	398	2	T35255	probable racemase
1336	63	4.6	400	2	C75336	enantiomer-selecti	1409	62.5	4.5	402	2	S37789	hypothetical prote
1337	63	4.6	403	2	H98327	hypothetical prote	1410	62.5	4.5	411	2	S71217	glutamate dehydrog
1338	63	4.6	418	2	T15142	paired box transcr	1411	62.5	4.5	427	2	S75210	glycine hydroxymet
1339	63	4.6	422	1	A56674	hypothetical prote	1412	62.5	4.5	450	2	E70681	probable trpE - My
1340	63	4.6	424	2	C86247	paired box transcr	1413	62.5	4.5	466	2	A87638	glutamate-1-semial
1341	63	4.6	428	2	T27544	zinc resistance pr	1414	62.5	4.5	473	2	A56175	adhesin plaque pr
1342	63	4.6	434	2	D96760	hypothetical prote	1415	62.5	4.5	478	2	S31906	beta-1,3-glucanase
1343	63	4.6	436	1	S42234	paired box transcr	1416	62.5	4.5	482	2	S76376	hypothetical prote





RESULT 6  
A53968  
serine proteinase SCCE precursor - human  
N;Alternate names: stratum corneum chymotryptic enzyme  
C;Species: Homo sapiens (man)

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RESULT 7
B25528
trypsin (EC 3.4.21.4) precursor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 09-Jul-2004
C:Accession: B25528
R:Stevenson, B.J.; Wollner, P.K.
Nucleic Acids Res. 14, 8307-8330, 1986
A:Title: Sequence organisation and transcriptional regulation of the mouse elastase II a
A:Reference number: A93646; MUID:87066713; PMID:3641189
A:Accession: B25528
A:Molecule type: mRNA
A:Residues: 1-246 <STE>
A:Cross-references: UNIPROT:P07146; GB:X04574; NID:G54918; PIDN:CAA28243.1; PID:G54919
C:Superfamily: trypsin; trypsin homology
C:Keywords: calcium binding; hydrolase; protein digestion; serine proteinase
F:1-23/Domain: signal sequence #status predicted <SIG>
F:24-246/Product: trypsin #status predicted <MAT>
F:24-239/Domain: trypsin homology <TRY>
F:30-160, 48-64, 132-233, 139-206, 171-185/Disulfide bonds: #status predicted
F:63, 107, 200/Active site: His, Asp, Ser #status predicted
F:75, 77, 80, 85/Binding site: Calcium (Glu, Asn, Val, Glu) #status predicted

Query Match 40.2%; Score 553; DB 2; Length 246;
Best Local Similarity 44.7%; Pred. No. 1.3e-37;
Matches 113; Conservative 45; Mismatches 81; Indels 14; Gaps 7;

Qy 3 LSIFLLCVLGSQA-----ATPKIFNGTEGRRNSQPQVGLFEGTSRLCGGVLIIDHRWVL 58
Db 1 MSALLILALVGAAPFVDDDDKIVGGYTCRSSVPVQSLNAGYHF-CGGLINDQWV 59

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QY 59 TAAHSGSRVYVRLGHSLSQLDWTQIRHSGFSVTHPGYLGASTSHEHDLRLRLPVP 118
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Db 60 SAAHCYKYRIQVRLGHNINVLGNEQFVDSAKIIRHPNY--NSWTLNDNDIMLIKASPV 117
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 119 RVTSSVQIPLPNDCCATAGTECHVSWG--ITNHPNRPFDLLQCLNLSIVSHATCHGVY 176
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 118 TLNARVASVPLPSSCAPAGTQCLISGWGNTLSGVNN--PDLLOCVDAFVLPQADCEASY 175
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 177 PGRITSNMVCAGVP--GQDACGDSGVLVCGVGLQGLVSGVSGPCGQDGPVGVYTYIC 235
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 176 PGDITNMICVGLLEGKDSQDGGPVCNGELQIVSWG--GCAQPDAPGVYTKVC 233
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 236 KYVDWIRMIMRNN 248
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 234 NYVDWIQNTIADN 246
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 8
TRBOTR
C:Species: Bos primigenius taurus (cattle)
N:Contents: trypsinogen
C:Species: Bos primigenius taurus (cattle)
C:Date: 24-Apr-1984 #sequence_revision 28-Feb-1986 #text_change 18-Jul-1997
R;Accession: A90164; A00946; S08774
R;Mikes, O.; Holeysovsky, V.; Tomasek, V.; Sorn, F.
Biochem. Biophys. Res. Commun. 24, 346-352, 1966
A:Title: Covalent structure of bovine trypsinogen. The position of the remaining amides.
A:Reference number: A90164; MUID:67168848; PMID:5967094
A:Accession: A90164
A:Molecule type: protein
A:Residues: 1-57,'Q',59-67,'Q',69-150,'N',152-176,'N',178-229 <MIK>
R;Hartley, B.S.
Philos. Trans. R. Soc. Lond. B257, 77-87, 1970
A:Reference number: A93755
A:Contents: annotation; revisions
A:Titani, K.; Ericsson, L.H.; Neurath, H.; Walsh, K.A.
Biochemistry 14, 1358-1366, 1975
A:Title: Amino acid sequence of dogfish trypsin.
A:Reference number: A00950; MUID:75146445; PMID:1092332
A:Contents: annotation; revisions
A:Note: the sequence agrees with that shown
R;Bode, W.; Schwager, P.
J. Mol. Biol. 98, 693-717, 1975
A:Title: The refined crystal structure of bovine beta-trypsin at 1.8 angstrom resolution.
A:Reference number: A92954; MUID:76072097; PMID:512
A:Contents: annotation; X-ray crystallography; binding sites for calcium, substrate, and
F;46,90,183/Active site: His, Asp, Ser #status experimental
C:Comment: Trypsinogen is synthesized in the acinar cells of the pancreas.
C:Comment: Autocatalytic cleavage after Lys-6 leads to beta-trypsin by releasing a terminal
pseudotrypsin. A cleavage may also occur after Arg-105.
C:Superfamily: trypsin; trypsin homology
C:Keywords: hydrolase; pancreas; protein digestion; serine proteinase; zymogen
F;1-229/Product: trypsinogen #status experimental <ZYM>
F;1-6/Domain: activation peptide #status experimental <APT>
F;7-222/Domain: trypsin homology <TRY>
F;7-131,132-229/Product: alpha-trypsin #status experimental <MPT>
F;6-7/Cleavage site: Lys-Ile (enteropeptidase) #status experimental
F;13-143,31-47,115-216,122-189,154-168,179-203/Disulfide bonds: #status experimental
F;46,90,183/Active site: His, Asp, Ser #status experimental
F;58,60,63,68/Binding site: Calcium (Glu, Asn, Val, Glu) #status experimental
F;131-132/Cleavage site: Lys-Ser (autolytic) #status experimental

Query Match 40.2%; Score 552; DB 1; Length 229;
Best Local Similarity 46.3%; Pred. No. 1.4e-37;
Matches 106; Conservative 40; Mismatches 77; Indels 6; Gaps 4;

QY 21 KIFNGTEGRNSQPNQVLFEGTSLRCGGVLIDHRWVLTAAHCSGRVYVRLGHSLSQL 80
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 6 KIVGYTCGANTVPQVSLNSGYHF--CGSLNSQWVVAACHYKSGIQVRLGEDNINV 64
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 81 DWTEQIRHSGFSVTHPGYLGASTSHEHDLRLRLPVRVTSVQIPLPNDCCATAGTEC 140
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 65 EGNEQFISASKSIVHPSY--NSNTLNNDIMLIKLSAASLNSRVASISLPTSCASAGTQC 122
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
```

```
QY 141 HVSWGITNHPNRPFDLLQCLNLSIVSHATCHGVYPCRITSNMVCAGVP--GQDACQGD 199
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 123 LISGNGNTKSSGTSPVDVLKCLKAPILSDSSCKSAIPQIITSNMFCAGYLGEGKDSQGD 182
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 200 SGGPLVCGVGLQGLVSGVSGPCGQDGPVGVYTYICKYVDWIRMIMRNN 248
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 183 SGGPVVCSGKLGIVSWG--GCAQKNKPGVYTKVCNVSVMIKQTIASN 229
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 9
TRBOTR
C:Species: Bos primigenius taurus (cattle)
N:Contents: trypsin (EC 3.4.21.4) - bovine
C:Date: 02-Dec-1993 #sequence_revision 03-Aug-1995 #text_change 09-Jul-2004
R;Accession: S13813
R;Le Huerou, I.; Wicker, C.; Guilloteau, P.; Toullec, R.; Puigserver, A.
Eur. J. Biochem. 193, 767-773, 1990
A:Title: Isolation and nucleotide sequence of cDNA clone for bovine pancreatic anionic trypsin.
A:Reference number: S13813; MUID:91065383; PMID:1701147
A:Accession: S13813
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-247 <HUE>
A:Cross-references: UNIPROT:Q29463; EMBL:X54703; NID:g829; PIDN:CAA38513.1; PID:g830
C:Superfamily: trypsin; trypsin homology
C:Keywords: hydrolase; protein digestion; serine proteinase
F;24-239/Domain: trypsin homology <TRY>
F;63,107,200/Active site: His, Asp, Ser #status predicted

Query Match 40.0%; Score 550; DB 2; Length 247;
Best Local Similarity 45.7%; Pred. No. 2.3e-37;
Matches 113; Conservative 40; Mismatches 84; Indels 10; Gaps 5;

QY 7 LLLCVLGLSQA----ATPKIFNGTEGRNSQPNQVLFEGTSLRCGGVLIDHRWVLTAAH 62
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 5 LILAFVGAFAVFPDSDDDKIVGGYTCAESVYPQVSLNAGYHF--CGSLNDNQWVVAH 63
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 63 CSGSRVYVRLGHSLSQLDWTQIRHSGFSVTHPGYLGASTSHEHDLRLRLPVRVTS 122
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 64 CYQYHIQVRLGEYNDVLEGGQFIDASKIIRHPKY--SSWTLNDNDILIKLSTPAVINA 121
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 123 SVQIPLPNDCCATAGTECHVSWGITNHPNRPFDLLQCLNLSIVSHATCHGVYPCRITS 182
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 122 RYSTLLPLSACASAGTECLISGNGNTLSSGVNYPDLLQCLVAPLLSHADCEASYPQIITN 181
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 183 NMVCAGVP--GQDACGDSGVLVCGVGLQGLVSGVSGPCGQDGPVGVYTYICKYVDWI 241
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 182 NMICAGLGGKDSQDGGPVCNGELQIVSWG--GCAQKNKPGVYTKVCNVVDWI 239
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 242 RMIMRNN 248
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 240 QETIAAN 246
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 10
TRBOTR
C:Species: Canis lupus familiaris (dog)
N:Alternate names: cationic trypsinogen
C:Species: Canis lupus familiaris (dog)
C:Date: 30-Sep-1987 #sequence_revision 30-Sep-1987 #text_change 09-Jul-2004
R;Accession: A26273
R;Pinsky, S.D.; LaForge, K.S.; Scheele, G.
Mol. Cell. Biol. 5, 2669-2676, 1985
A:Title: Differential regulation of trypsinogen mRNA translation: full-length mRNA sequence
A:Reference number: A26273; MUID:86284628; PMID:3841794
A:Accession: A26273
A:Molecule type: mRNA
A:Residues: 1-247 <PIN>
A:Cross-references: UNIPROT:P06872; GB:M11589; NID:g164084; PIDN:AAA30899.1; PID:g164095
C:Superfamily: trypsin; trypsin homology
C:Keywords: hydrolase; pancreas; protein digestion; serine proteinase; zymogen
F;1-15/Domain: signal sequence #status predicted <SIG>
```

F;16-23/Domain: activation peptide #status predicted <APT>  
F;24-247/Product: trypsin, anionic #status predicted <ENZ>  
F;24-239/Domain: trypsin homology <TRY>  
F;30-160,48-64,132-233,139-206,171-185/disulfide bonds: #status predicted  
F;63,107,200/Active site: His, Asp, Ser #status predicted  
F;75,77,80,85/Binding site: calcium (Glu, Asn, Val, Glu) #status predicted

Query Match 39.7%; Score 546; DB 1; Length 247;  
Best Local Similarity 45.6%; Pred. No. 4.8e-37;  
Matches 113; Conservative 38; Mismatches 85; Indels 12; Gaps 6;

Qy 7 LLLCVLGLSQAATP-----KIFNGTECGRNSQPWQVGLFEGETSLRCGGVLIDHRWLTA 61  
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |  
Db 5 LLIAFLG-AAVAFTPTDDDDKI VGYTTCENSVFPQVSLNAGYHF-CGGSLISDQVVVSA 62  
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |  
Qy 62 HCSGRVWWELGHSLSQLDWTEQIRHSGFSVTHPGYLGASTSHEDLRLRLPLRVVT 121  
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |  
Db 63 HCYSKRIVQRVLGEYNIDVLEGNQFINSAKVIRHPNY--NSWLNDNDIMLIKUSSPAVLN 120  
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |  
Qy 122 SSVQPLPLPNDCCATAGTECHVSWGMIITNHPRNPFPDLLOCLNLISIVSHATCHGVYPERIT 181  
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |  
Db 121 ARVATTISLPRAAAGTGQCILSCGWNTLSGGTYNPPELLQCLDAPILTQAQCEASYFGQIT 180  
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |  
Qy 182 SNMVCAGGVP-GQDACGDGSGPLVCGGVVLQGLVSWGSVGPCGQDGIPGVYTVICKVDW 240  
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |  
Db 181 ENMICAGLEGKKDSQCGDSGPVNCDELQGIWSGY--GCAQKNKPGVYTKVCNFVDW 238  
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |  
Qy 241 IRMIMRN 248  
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |  
Db 239 IQSTIAAN 246  
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

RESULT 11  
TRDCG  
trypsin (EC 3.4.21.4) precursor, cationic - dog  
N;Alternate names: cationic trypsinogen  
C;Species: Canis lupus familiaris (dog)  
C;Date: 30-Sep-1987 #sequence\_revision 30-Sep-1987 #text\_change 09-Jul-2004  
C;Accession: B26273  
R;Pinsky, S.D.; LaForge, K.S.; Scheele, G.  
Mol. Cell. Biol. 5, 2669-2676, 1985  
A;Title: Differential regulation of trypsinogen mRNA translation: full-length mRNA sequence  
A;Reference number: A26273; MUID:86284628; PMID:3841794  
A;Accession: B26273  
A;Molecule type: mRNA  
A;Residues: 1-246 <PIN>  
A;Cross-references: UNIPROT:P06871; GB:M11590; NID:g164096; PIDN:AAA30900.1; PID:g164097  
C;Superfamily: trypsin; trypsin homology  
C;Keywords: hydrolase; pancreas; protein digestion; serine proteinase; zymogen  
F;1-15/Domain: signal sequence #status predicted <SIG>  
F;16-23/Domain: activation peptide #status predicted <APT>  
F;24-246/Product: trypsin, cationic #status predicted <ENZ>  
F;24-239/Domain: trypsin homology <TRY>  
F;30-160,48-64,132-233,139-206,171-185/disulfide bonds: #status predicted  
F;63,107,200/Active site: His, Asp, Ser #status predicted  
F;75,77,80,85/Binding site: calcium (Glu, Asn, Val, Glu) #status predicted

	Query Match	39.7%;	Score 545;	DB 1;	Length 246;	
	Best Local Similarity	44.2%;	Pred. No. 5.8e-37;			
	Matches 111;	Conservative 43;	Mismatches 87;	Indels 10;	Gaps 6;	
Qy	3	LSIFLLLCVLGLSQA----	ATPKLFNGTECCRN SQPQVGLFEGTSLRCGGVLIDHRWL	58		
	:	:	:	:	:	:
Dd	1	MKTFIFALGATVAFPIDDDKIVGVYTCGRNSVPYQVSLSNGVHP-CGSGLINSQWVV	59			
	:	:	:	:	:	:
Qy	59	TAAHCSGRYWVRIGHSLSQLDWTETQIRHSGFSVTHPGYLGASTSHHEHDRLRLRPV	118			
	:	:	:	:	:	:
Dd	60	SAAHCYSRIQVRLGEYNIAVSEGEQFINAAKIIRHPRY-NANTI-DNDIMLIKLSPPA	117			
	:	:	:	:	:	:
Qy	119	RVTSSVQPLPLPNDCATAGTCHSVGWGITNHPNPFPDLLLOCLNLSIVSHATCHGVYPG	178			
	:	:	:	:	:	:
Dd	118	TLSNRVSAIALPKSCPAAGTCLISGHWGNTQSIGONTPDVLOCIKAPILSDVCVRNAYPG	177			
	:	:	:	:	:	:

```

179 RITSNWCAGVP--QDACAQSGSGGLVCGGVVLQGLVSWGSGVPGCGDGIQGVVYICKY 237
   Q:|||||:|:|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
178 QISSNMCLGYMEGKSGQSGSGGFWVCNGELQGVVSWGA--GCAQKRGVSPKVCKY 235
   Q:|||||:|:|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

238 VDWMIMMNN 248
   V:|||||:|:|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
236 VSWIQQTAAAN 246
   V:|||||:|:|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 12
A27547
C:trypsin (EC 3.4.21.4) precursor, cationic - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 09-Jul-2004
C:Accession: A27547
R:Fletcher, T.S.; Alhadeff, M.; Craik, C.S.; Largman, C.
Biochemistry 26, 3081-3086, 1987
A:Title: Isolation and characterization of a cDNA encoding rat cationic trypsinogen.
A:Reference number: A27547; MUID:87271609; PMID:3607011
A:Accession: A27547
A:Molecule type: mRNA
A:Residues: 1-247 <FILE>
A:Cross-references: UNIPROT:P08426; GB:M16624; NID:g206498; PIDN:AAA41985.1; PID:g206499
C:Superfamily: trypsin; trypsin homology
C:Keywords: calcium binding; hydrolase; protein digestion; serine proteinase
F/23-240/Domain: trypsin homology <TRY>
F/31-161,49-65,133-234,140-207,172-186/Disulfide bonds: #status predicted
F/64,108,201/Active site: His, Asp, Ser #status predicted
F/76,78,81,86/Binding site: calcium (Glu, Asn, Val, Glu) #status predicted

```

Query Match	39.6%	Score 544.5;	DB 2;	Length 247;
Best Local Similarity	43.3%;	Pred. No. 6.3e-37;		
Matches 109;	Conservative	43;	Mismatches 89;	Indels 11;
				Gaps 5;

Qy	3	LSIFLLCVLGLSQAA-----TPKIFNGTECGRNSOPQWGLPEGTSLRCGGVLIDHRWV	57
Db	1	MKALIFLAFAGAAVALPLDDDDDKIVGGYTCQKNSLPYQVSLNAGYHF-CGGSILNSQWV	59
Qy	58	LTAHCGSGRYWYRLGEHSLSQLSDWTQEIHRHSGFVTHPCYLGASTSHEHDLRLRLRLP	117
Db	60	VSAHCVKSRIVQRLGEHNIDVGEGEQFIDAAKIIRHPSY--NANTFDNDIMLIKLNSP	117
Qy	118	VRVTSYVQPLPLPNDCATAGTECHVSGWGTINHRNPFDPDLLQCLNLSIVSHATCHGVYP	177
Db	118	ATLNSRVSTVSLPRSCGSSGKTCLVSGWGNLTSSGTNYPSLLQCLDAPVLSDSSCKSSYP	177
Qy	178	GRITSNMVCAGGYP-GQDACQGSGGPLVCGGVLQGLVSMGVSGPCQGDGIPGVYTYICK	236
Db	178	GKITSNMFLGFLIEGGKDCQGSJGGPVVNCNQLQGVVSMGY--GCAQKKGPGVYTKVCN	235
Qy	237	YVDWIRMIMRNN	248
Db	236	YVNWIOOTVAAN	247

RESULT 13  
TRBT1

trypsin (EC 3.4.21.4) I precursor - rat  
N;Alternate names: trypsinogen I  
C;Species: Rattus norvegicus (Norway rat)  
C;Date: 17-Dec-1982 #sequence\_revision 17-Dec-1982 #text\_change 09-Jul-2004  
C;Accession: B22657; A00948  
R;Craik, C.S.; Choo, Q.L.; Swift, G.H.; Quinto, C.; MacDonald, R.J.; Rutter, W.J.  
J. Biol. Chem. 259, 14255-14264, 1984  
A;Title: Structure of two related rat pancreatic trypsin genes.  
A;Reference number: A22657; MUID:85054880; PMID:6094547  
A;Accession: B22657  
A;Molecule type: DNA  
A;Residues: 1-246 <CRA>  
A;Cross-references: UNIPROT:P00762; GB:J00778; NID:G206507; PIDN:AAA98518.1; PID:G206508  
A;Note: the authors translated the codon ATC for residue 6 as Leu and GAC for residue 17  
R;MacDonald, R.J.; Stary, S.J.; Swift, G.H.  
J. Biol. Chem. 257, 9724-9732, 1982

A;Title: Two similar but nonallelic rat pancreatic trypsinogens. Nucleotide sequences of  
A;Reference number: A00948; MUID:82265624; PMID:6896710  
A;Accession: A00948  
A;Molecule type: mRNA  
A;Cross-references: GB:J00778; NID:g206507; PIDN:AAA98518.1; PID:g206508  
C;Genetics:  
A;Introns: 14/1; 67/2; 152/1; 197/3  
C;Superfamily: trypsin; trypsin homology  
C;Keywords: hydrolase; pancreas; protein digestion; serine proteinase; zymogen  
F;1-15/Domain: signal sequence #status predicted <SIG>  
F;16-23/Domain: activation peptide #status predicted <APT>  
F;24-246/Product: trypsin I #status predicted <ENZ>  
F;24-239/Domain: trypsin homology <TRY>  
F;30-160,48-64,132-233,139-206,171-185/Disulfide bonds: #status predicted  
F;63,107,200/Active site: His, Asp, Ser #status predicted  
F;75,77,80,85/Binding site: calcium (Glu, Asn, Val, Glu) #status predicted

Query Match 39.3%; Score 540; DB 1; Length 246;  
Best Local Similarity 44.5%; Pred. No. 8.4e-37;  
Matches 110; Conservative 47; Mismatches 76; Indels 14; Gaps 7;

QY 3 LSTPILLVGLSLQA----ATPKIFNGTEGCRNSQPMQVGLFEGTSLRCGVLIDHRWL 58  
DB 1 MSALLILALVGAAPLEDDDKIVGGYTCPEHSVPYQVSLNSGYHF-CGSLINDQWV 59

QY 59 TAAHCSGRYWRVLGHSLSQLDWTQIRHSGFSVTHPGYLGASTSHEHDLRLRLPV 118  
DB 60 SAAHCYKSRIQVRLGHNINVLGDSQFINAAKIIKHPNY--SSWTLNDIMLIKSSPV 117

QY 119 RVTSSVQPLPNDTCATAGTECHVSQWG--ITNHRPNPFDLLQCLNLSIVSHATCGVY 176  
DB 118 KLNARVAPVALPACAPAGTQCLISGNTLSGVNN--PDLLQCVDAVLSQDCEAY 175

QY 177 PGRITNMVCAQGVV-GQDACQDGGSLVCGVGLQGLVSWGSGVCGQDGIQVYTYIC 235  
DB 176 PGRITSMICVGLGEGKDSQDGGVVCNGQLQGIWSGY--GCALPDNPGVYTKVC 233

QY 236 KYVDWIR 242  
DB 234 NFVGWIQ 240

RESULT 14  
S31779  
trypsin (EC 3.4.21.4) III precursor - Atlantic salmon (fragment)  
C;Species: Salmo salar (Atlantic salmon)  
C;Date: 22-Nov-1993 #sequence\_revision 03-Aug-1995 #text\_change 09-Jul-2004  
C;Accession: S66657; S31779  
R;Male, R.; Lorens, J.B.; Smalas, A.O.; Torrisen, K.R.  
Eur. J. Biochem. 232, 677-685, 1995  
A;Title: Molecular cloning and characterization of anionic and cationic variants of trypsin  
A;Reference number: S66657; MUID:96035908; PMID:7556223  
A;Accession: S66657  
A;Molecule type: mRNA  
A;Residues: 1-238 <MAL>  
A;Cross-references: UNIPROT:P35033; EMBL:X70074; NID:g64387; PIDN:CAA49679.1; PID:g64388  
C;Superfamily: trypsin; trypsin homology  
C;Keywords: hydrolase; serine proteinase  
F;1-7/Domain: signal sequence (fragment) #status predicted <SIG>  
F;8-15/Domain: activation peptide #status predicted <APT>  
F;16-238/Product: trypsin III #status predicted <MAT>  
F;16-231/Domain: trypsin homology <TRY>  
F;22-152,40-56,124-225,131-198,163-177,188-212/Disulfide bonds: #status predicted  
F;55,99,192/Active site: His, Asp, Ser #status predicted

Query Match 39.3%; Score 540; DB 2; Length 238;  
Best Local Similarity 47.2%; Pred. No. 1.4e-36;  
Matches 108; Conservative 37; Mismatches 78; Indels 6; Gaps 4;

QY 21 KIFNGTEGCRNSQPMQVGLFEGTSLRCGVLIDHRVLTAAHCSGRYWRVLGHSLSQ 80  
DB 15 KIVGGYECRKNASQASQSGYHF-CGGLISSTWVWSAAHCYKRIQVRLGHNIAV 73

QY 81 DWTEQIRHSGFSVTHPGYLGASTSHEHDLRLRLPVRTVTSVQPLPNDTCATGTC 140  
DB 74 EGTEQFIDSVKVMHPSY--NSRLNDIMLIKSLFASLNSVSVLPSSCASSSTRC 131

QY 141 HVSQGWGITHRPNPFPDILLQCLNLSIVSHATCGVTPGRITSNMVCAGVVP-GQDACQGD 199  
DB 132 LVSGWGNLSSGSSNYPDTLRCLDLPILSSSSCNASYPGQITSNWFCAGFEGGKDSQGD 191

QY 200 SGGLVCGVGLQGLVSWGSGVCGQDGIQGVYTYICKYVDWIRIMRN 248  
DB 192 SGFPVVCNGQLQGLVSWGY--GCAQRNKGVTYKVCNYSRWSWISSTSSN 238

RESULT 15  
S05494  
trypsin (EC 3.4.21.4) IV precursor - rat  
N;Alternate names: 23K protein; trypsinogen IV precursor  
C;Species: Rattus norvegicus (Norway rat)  
C;Date: 07-Jun-1990 #sequence\_revision 07-Jun-1990 #text\_change 09-Jul-2004  
C;Accession: S05494  
R;Juetcker, H.; Rausch, U.; Vasiloudes, P.; Scheele, G.A.; Kern, H.F.  
Nucleic Acids Res. 17, 6736, 1989  
A;Title: A fourth trypsinogen (P23) in the rat pancreas induced by CCK.  
A;Reference number: S05494; MUID:89386010; PMID:2780302  
A;Accession: S05494  
A;Molecule type: mRNA  
A;Residues: 1-247 <LUE>  
A;Cross-references: UNIPROT:P12788; EMBL:X15679; NID:g56813; PIDN:CAA33718.1; PID:g56814  
C;Superfamily: trypsin; trypsin homology  
C;Keywords: calcium binding; hydrolase; protein digestion; serine proteinase; zymogen  
F;1-15/Domain: signal sequence #status predicted <SIG>  
F;16-23/Domain: activation peptide #status predicted <APT>  
F;24-247/Product: trypsin IV #status predicted <MAT>  
F;24-240/Domain: trypsin homology <TRI>  
F;30-161,49-65,133-334,140-207,172-186/Disulfide bonds: #status predicted  
F;64,108,201/Active site: His, Asp, Ser #status predicted  
F;76,78,81,86/Binding site: calcium (Glu, Asn, Val, Glu) #status predicted

Query Match 38.8%; Score 533.5; DB 2; Length 247;  
Best Local Similarity 43.4%; Pred. No. 4.9e-36;  
Matches 109; Conservative 41; Mismatches 94; Indels 7; Gaps 4;

QY 1 MGLSIF--LILLCVLGLSQAATPKIFNGTEGCRNSQPMQVGLFEGTSLRCGVLIDHRWL 58  
DB 1 MKTISFFAFLGAVALPVNDDDKIVGGYTCPEHLVPVQVSLHDGISHQCGSLSDQWL 60

QY 59 TAAHCSGRYWRVLGHSLSQLDWTQIRHSGFSVTHPGYLGASTSHEHDLRLRLPV 118  
DB 61 SAAHCYKRIQVRLGHNINVLGEGSQFIDAEEKIIRHPEY--NKDTLDNDIMLIKSP 118

QY 119 RVTSSVQPLPNDTCATAGTECHVSQWGITHRPNPFPDILLQCLNLSIVSHATCGVYPG 178  
DB 119 VLNSQVSTSLPRSCASTDAQCLVSWGNTVSTGGKYPALLQCLLEAPVLSASCKKSYPG 178

QY 179 RITSNMVCAGVVP-GQDACQDGGSLVCGVGLQGLVSWGSGVCGQDGIQGVYTYCKY 237  
DB 179 QITSNMFCFLGEGKDSQDGGVVCNGEIQGVSWGSV--CAMRGKPGVYTKVCNY 236

QY 238 VDWIRIMRN 248  
DB 237 LSWIQETMANN 247

Search completed: March 5, 2005, 17:59:08  
Job time : 53 secs



OM protein - protein search, using sw model  
 Run on: March 5, 2005, 17:55:12 ; Search time 165 Seconds  
 (without alignments)  
 581.313 Million cell updates/sec

Title: US-10-006-856A-194  
 Perfect score: 1374  
 Sequence: 1 MGSIFFLLCVLGLSQAATP.....GVVYICKYVDWIRIMRNN 248  
 Scoring table: BLOSUM62  
 Gapop 10.0 ; Gapext 0.5  
 Searched: 2105692 seqs, 386760381 residues  
 Total number of hits satisfying chosen parameters: 2105692  
 Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000  
 Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 1500 summaries  
 A\_Geneseq\_16Dec04:\*

- 1: Geneseq1980s:\*
- 2: Geneseq1990s:\*
- 3: Geneseq2000s:\*
- 4: Geneseq2001s:\*
- 5: Geneseq2002s:\*
- 6: Geneseq2003as:\*
- 7: Geneseq2003bs:\*
- 8: Geneseq2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

No.	Score	Match	Length	DB	ID	Description
RESULT 1						SUMMARIES
ID	AAB21304	standard; protein; 248 AA.				
DE	Human KIX-L5 protein #4.					
PN	WO200053776-A2.					
PD	14-SEP-2000.					
PA	(MOUN) MOUNT SINAI HOSPITAL.					
Query Match	100.0%;	Score 1374;	DB 3;	Length 248;		
Best Local Similarity	100.0%;	Pred. No. 5e-98;				
RESULT 2						
ID	AAB24428	standard; protein; 248 AA.				
DE	Human PRO1303 protein sequence SEQ ID NO:203.					
PN	WO200032221-A2.					
PD	08-JUN-2000.					
PA	(GETH) GENENTECH INC.					
Query Match	100.0%;	Score 1374;	DB 3;	Length 248;		
Best Local Similarity	100.0%;	Pred. No. 5e-98;				
RESULT 3						
ID	AAB24032	standard; protein; 248 AA.				
DE	Human PRO1303 protein sequence SEQ ID NO:33.					
PN	WO200053750-A1.					
PD	14-SEP-2000.					
PA	(GETH) GENENTECH INC.					
Query Match	100.0%;	Score 1374;	DB 3;	Length 248;		
Best Local Similarity	100.0%;	Pred. No. 5e-98;				
RESULT 4						
ID	AA99393	standard; protein; 248 AA.				
DE	Human PRO1303 (UNQ669) amino acid sequence SEQ ID NO:194.					
PN	WO200012708-A2.					
PD	09-MAR-2000.					
PA	(GETH) GENENTECH INC.					
Query Match	100.0%;	Score 1374;	DB 3;	Length 248;		
Best Local Similarity	100.0%;	Pred. No. 5e-98;				
RESULT 5						
ID	AA23994	standard; protein; 248 AA.				
DE	Human EST encoded protein SEQ ID NO: 1519.					
PN	WO200154477-A2.					
PD	02-AUG-2001.					
PA	(HYSE-) HYSEQ INC.					
Query Match	100.0%;	Score 1374;	DB 4;	Length 248;		
Best Local Similarity	100.0%;	Pred. No. 5e-98;				
RESULT 6						
ID	AAB66142	standard; protein; 248 AA.				

DE Protein of the invention #54.  
 PN WO200078961-A1.  
 PD 28-DEC-2000.  
 PA (GETH) GENENTECH INC.  
 Query Match 100.0%; Score 1374; DB 4; Length 248;  
 Best Local Similarity 100.0%; Pred. No. 5e-98;

RESULT 7

ID ABO33635 standard; protein; 248 AA.  
 DE Novel human secreted and transmembrane protein PRO1303.  
 PN US2003073130-A1.  
 PD 17-APR-2003.  
 PA (GETH) GENENTECH INC.  
 Query Match 100.0%; Score 1374; DB 6; Length 248;  
 Best Local Similarity 100.0%; Pred. No. 5e-98;

RESULT 8

ID ABO44488 standard; protein; 248 AA.  
 DE Human secreted/transmembrane protein PRO1303.  
 PN US2003044841-A1.  
 PD 06-MAR-2003.  
 PA (GETH) GENENTECH INC.  
 Query Match 100.0%; Score 1374; DB 7; Length 248;  
 Best Local Similarity 100.0%; Pred. No. 5e-98;

RESULT 9

ID ABO33512 standard; protein; 248 AA.  
 DE Novel human secreted and transmembrane protein PRO1303.  
 PN US2003073129-A1.  
 PD 17-APR-2003.  
 PA (GETH) GENENTECH INC.  
 Query Match 100.0%; Score 1374; DB 7; Length 248;  
 Best Local Similarity 100.0%; Pred. No. 5e-98;

RESULT 10

ID ADC18063 standard; protein; 248 AA.  
 DE Human PRO polypeptide #54.  
 PN US2003064925-A1.  
 PD 03-APR-2003.  
 PA (GETH) GENENTECH INC.  
 Query Match 100.0%; Score 1374; DB 7; Length 248;  
 Best Local Similarity 100.0%; Pred. No. 5e-98;

RESULT 11

ID ADD70709 standard; protein; 248 AA.  
 DE Human secreted/transmembrane protein PRO1303.  
 PN US2003099625-A1.  
 PD 29-MAY-2003.  
 PA (GETH) GENENTECH INC.  
 Query Match 100.0%; Score 1374; DB 7; Length 248;  
 Best Local Similarity 100.0%; Pred. No. 5e-98;

RESULT 12

ID ADD39786 standard; protein; 248 AA.  
 DE Human secreted/transmembrane protein PRO1303.  
 PN US2003083462-A1.  
 PD 01-MAY-2003.  
 PA (GETH) GENENTECH INC.  
 Query Match 100.0%; Score 1374; DB 7; Length 248;  
 Best Local Similarity 100.0%; Pred. No. 5e-98;

RESULT 13

ID ADD70232 standard; protein; 248 AA.  
 DE Human secreted/transmembrane protein PRO1303.  
 PN US2003054406-A1.  
 PD 20-MAR-2003.  
 PA (GETH) GENENTECH INC.  
 Query Match 100.0%; Score 1374; DB 7; Length 248;  
 Best Local Similarity 100.0%; Pred. No. 5e-98;

RESULT 14

ID ADD38353 standard; protein; 248 AA.  
 DE Human secreted/transmembrane protein PRO1303.  
 PN US2003096955-A1.  
 PD 22-MAY-2003.  
 PA (GETH) GENENTECH INC.  
 Query Match 100.0%; Score 1374; DB 7; Length 248;  
 Best Local Similarity 100.0%; Pred. No. 5e-98;

RESULT 15

ID ADD39309 standard; protein; 248 AA.  
 DE Human secreted/transmembrane protein PRO1303.

PN US2003096954-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1374; DB 7; Length 248;  
Best Local Similarity 100.0%; Pred. No. 5e-98;  
RESULT 16  
ID ADE96567 standard; protein; 248 AA.  
DE Human secreted/transmembrane protein PRO1303.  
PN US2003092061-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1374; DB 7; Length 248;  
Best Local Similarity 100.0%; Pred. No. 5e-98;  
RESULT 17  
ID ADF25878 standard; protein; 248 AA.  
DE Human secreted/transmembrane protein PRO1303.  
PN US2003082627-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1374; DB 7; Length 248;  
Best Local Similarity 100.0%; Pred. No. 5e-98;  
RESULT 18  
ID ADE50484 standard; protein; 248 AA.  
DE Human secreted/transmembrane protein PRO1303.  
PN US2003069179-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1374; DB 7; Length 248;  
Best Local Similarity 100.0%; Pred. No. 5e-98;  
RESULT 19  
ID ADE20096 standard; protein; 248 AA.  
DE Human secreted/transmembrane protein PRO1303.  
PN US2003092883-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1374; DB 7; Length 248;  
Best Local Similarity 100.0%; Pred. No. 5e-98;  
RESULT 20  
ID ADE50007 standard; protein; 248 AA.  
DE Human secreted/transmembrane protein PRO1303.  
PN US2003082626-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1374; DB 7; Length 248;  
Best Local Similarity 100.0%; Pred. No. 5e-98;  
RESULT 21  
ID ADE21565 standard; protein; 248 AA.  
DE Human secreted/transmembrane protein PRO1303.  
PN US2003082628-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1374; DB 7; Length 248;  
Best Local Similarity 100.0%; Pred. No. 5e-98;  
RESULT 22  
ID ADF29990 standard; protein; 248 AA.  
DE Human secreted/transmembrane protein PRO1303.  
PN US2003204053-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1374; DB 7; Length 248;  
Best Local Similarity 100.0%; Pred. No. 5e-98;  
RESULT 23  
ID ADF55883 standard; protein; 248 AA.  
DE Human secreted/transmembrane protein PRO1303.  
PN US2003204054-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1374; DB 7; Length 248;  
Best Local Similarity 100.0%; Pred. No. 5e-98;  
RESULT 24  
ID ADH99387 standard; protein; 248 AA.  
DE Human secreted/transmembrane protein PRO1303.  
PN US2003065142-A1.

PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1374; DB 7; Length 248;  
Best Local Similarity 100.0%; Pred. No. 5e-98;  
RESULT 25  
ID ADE96567 standard; protein; 248 AA.  
DE Human secreted/transmembrane protein PRO1303.  
PN US2003195347-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1374; DB 8; Length 248;  
Best Local Similarity 100.0%; Pred. No. 5e-98;  
RESULT 26  
ID ADF25878 standard; protein; 248 AA.  
DE Human secreted/transmembrane protein PRO1303.  
PN US2003199675-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1374; DB 8; Length 248;  
Best Local Similarity 100.0%; Pred. No. 5e-98;  
RESULT 27  
ID ADF24777 standard; protein; 248 AA.  
DE Human secreted/transmembrane protein PRO1303.  
PN US2003198993-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1374; DB 8; Length 248;  
Best Local Similarity 100.0%; Pred. No. 5e-98;  
RESULT 28  
ID ADF29513 standard; protein; 248 AA.  
DE Human secreted/transmembrane protein PRO1303.  
PN US2003203401-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1374; DB 8; Length 248;  
Best Local Similarity 100.0%; Pred. No. 5e-98;  
RESULT 29  
ID ADE97044 standard; protein; 248 AA.  
DE Human secreted/transmembrane protein PRO1303.  
PN US2003195334-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1374; DB 8; Length 248;  
Best Local Similarity 100.0%; Pred. No. 5e-98;  
RESULT 30  
ID ADH03082 standard; protein; 248 AA.  
DE Human secreted/transmembrane protein PRO1303.  
PN US2003216562-A1.  
PD 20-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1374; DB 8; Length 248;  
Best Local Similarity 100.0%; Pred. No. 5e-98;  
RESULT 31  
ID ADH04036 standard; protein; 248 AA.  
DE Human secreted/transmembrane protein PRO1303.  
PN US2003220471-A1.  
PD 27-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1374; DB 8; Length 248;  
Best Local Similarity 100.0%; Pred. No. 5e-98;  
RESULT 32  
ID ADH03559 standard; protein; 248 AA.  
DE Human secreted/transmembrane protein PRO1303.  
PN US2003224478-A1.  
PD 04-DEC-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1374; DB 8; Length 248;  
Best Local Similarity 100.0%; Pred. No. 5e-98;  
RESULT 33  
ID ADH04513 standard; protein; 248 AA.  
DE Human secreted/transmembrane protein PRO1303.  
PN US2004005626-A1.  
PD 08-JAN-2004.

PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1374; DB 8; Length 248;  
Best Local Similarity 100.0%; Pred. No. 5e-98;  
RESULT 34  
ID ADH61514 standard; protein; 248 AA.  
DE Human secreted/transmembrane protein PRO1303.  
PN US2004014130-A1.  
PD 22-JAN-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1374; DB 8; Length 248;  
Best Local Similarity 100.0%; Pred. No. 5e-98;  
RESULT 35  
ID ADN10927 standard; protein; 248 AA.  
DE Human kallikrein 12, marker of endocrine cancer.  
PN WO2004029285-A2.  
PD 08-APR-2004.  
PA (MOUN ) MOUNT SINAI HOSPITAL.  
Query Match 100.0%; Score 1374; DB 8; Length 248;  
Best Local Similarity 100.0%; Pred. No. 5e-98;  
RESULT 36  
ID ADL94713 standard; protein; 248 AA.  
DE Human secreted/transmembrane protein PRO1303.  
PN US2004073015-A1.  
PD 15-APR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1374; DB 8; Length 248;  
Best Local Similarity 100.0%; Pred. No. 5e-98;  
RESULT 37  
ID ADT94373 standard; protein; 248 AA.  
DE Human PRO1303 protein.  
PN AU2003259607-A1.  
PD 27-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1374; DB 8; Length 248;  
Best Local Similarity 100.0%; Pred. No. 5e-98;  
RESULT 38  
ID AAO29516 standard; protein; 248 AA.  
DE Human kallikrein-like protein 5 (18817).  
PN WO2003039475-A2.  
PD 15-MAY-2003.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 99.5%; Score 1367; DB 6; Length 248;  
Best Local Similarity 99.6%; Pred. No. 1.7e-97;  
RESULT 39  
ID AAB21303 standard; protein; 254 AA.  
DE Human KLK-L5 protein #3.  
PN WO200053776-A2.  
PD 14-SEP-2000.  
PA (MOUN ) MOUNT SINAI HOSPITAL.  
Query Match 94.7%; Score 1301; DB 3; Length 254;  
Best Local Similarity 100.0%; Pred. No. 2.2e-92;  
RESULT 40  
ID ABG66676 standard; protein; 254 AA.  
DE Human novel polypeptide #11.  
PN WO200244340-A2.  
PD 06-JUN-2002.  
PA (HYSE-) HYSEQ INC.  
Query Match 94.7%; Score 1301; DB 5; Length 254;  
Best Local Similarity 100.0%; Pred. No. 2.2e-92;  
RESULT 41  
ID ADN10926 standard; protein; 254 AA.  
DE Human kallikrein 12, marker of endocrine cancer.  
PN WO2004029285-A2.  
PD 08-APR-2004.  
PA (MOUN ) MOUNT SINAI HOSPITAL.  
Query Match 94.7%; Score 1301; DB 8; Length 254;  
Best Local Similarity 100.0%; Pred. No. 2.2e-92;  
RESULT 42  
ID ADP56174 standard; protein; 254 AA.  
DE Human PRO protein sequence SEQ ID NO:2150.  
PN WO2004039956-A2.  
PD 13-MAY-2004.  
PA (GETH ) GENENTECH INC.

Query Match 94.7%; Score 1301; DB 8; Length 254;  
Best Local Similarity 100.0%; Pred. No. 2.2e-92;  
RESULT 43  
ID AAB21301 standard; protein; 184 AA.  
DE Human KLK-L5 protein #1.  
PN WO200053776-A2.  
PD 14-SEP-2000.  
PA (MOUN ) MOUNT SINAI HOSPITAL.  
Query Match 74.2%; Score 1019; DB 3; Length 184;  
Best Local Similarity 100.0%; Pred. No. 8.5e-71;  
RESULT 44  
ID AAY28642 standard; protein; 162 AA.  
DE Human secreted protein from cDNA clone HKAFV61.  
PN WO9940183-A1.  
PD 12-AUG-1999.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 59.0%; Score 811; DB 2; Length 162;  
Best Local Similarity 64.1%; Pred. No. 8.1e-55;  
RESULT 45  
ID AAY32852 standard; protein; 260 AA.  
DE Human serine protease protein sequence.  
PN JP11225765-A.  
PD 24-AUG-1999.  
PA (SUNR ) SUNTORY LTD.  
Query Match 45.9%; Score 630.5; DB 2; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 46  
ID AAY41744 standard; protein; 260 AA.  
DE Human PRO322 protein sequence.  
PN WO9946281-A2.  
PD 16-SEP-1999.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 2; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 47  
ID AAY03220 standard; protein; 260 AA.  
DE Amino acid sequence of human tumour antigen derived gene-14 protein.  
PN WO9909138-A1.  
PD 25-FEB-1999.  
PA (UYAR-) UNIV ARKANSAS.  
Query Match 45.9%; Score 630.5; DB 2; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 48  
ID AAB21322 standard; protein; 260 AA.  
DE Human neuropsin.  
PN WO200053776-A2.  
PD 14-SEP-2000.  
PA (MOUN ) MOUNT SINAI HOSPITAL.  
Query Match 45.9%; Score 630.5; DB 3; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 49  
ID AAB43300 standard; protein; 260 AA.  
DE Human PRO322 (UNQ283) protein sequence SEQ ID NO:395.  
PN WO200053756-A2.  
PD 14-SEP-2000.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 3; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 50  
ID AAY51131 standard; protein; 260 AA.  
DE Human neuropsin protein.  
PN JP11318461-A.  
PD 24-NOV-1999.  
PA (SHIO/) SHIOZAKA S.  
Query Match 45.9%; Score 630.5; DB 3; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 51  
ID AAU12369 standard; protein; 260 AA.  
DE Human PRO322 polypeptide sequence.  
PN WO200140466-A2.  
PD 07-JUN-2001.  
PA (GETH ) GENENTECH INC.

Query Match 45.9%; Score 630.5; DB 4; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 52  
ID AAB53087 standard; protein; 260 AA.  
DE Human angiogenesis-associated protein PRO322, SEQ ID NO:127.  
PN WO200053753-A2.  
PD 14-SEP-2000.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 4; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 53  
ID ABG23373 standard; protein; 260 AA.  
DE Novel human diagnostic protein #23364.  
PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 45.9%; Score 630.5; DB 4; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 54  
ID ABB84852 standard; protein; 260 AA.  
DE Human PRO322 protein sequence SEQ ID NO:72.  
PN WO200200690-A2.  
PD 03-JAN-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 5; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 55  
ID AAU81959 standard; protein; 260 AA.  
DE Human PRO322.  
PN WO200109327-A2.  
PD 08-FEB-2001.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 5; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 56  
ID ABB95458 standard; protein; 260 AA.  
DE Human angiogenesis related protein PRO322 SEQ ID NO: 72.  
PN WO200208284-A2.  
PD 31-JAN-2002.  
PA (GETH ) GENENTECH INC.  
PA (BAKE/) BAKER K P.  
PA (FERR/) FERRARA N.  
PA (GERB/) GERBER H.  
PA (GERR/) GERRITSEN M E.  
PA (GODD/) GODDARD A.  
PA (GODO/) GODOWSKI P J.  
PA (GURN/) GURNEY A L.  
PA (HILL/) HILLAN K J.  
PA (MARS/) MARSTERS S A.  
PA (PANJ/) PAN J.  
PA (PAON/) PAONI N F.  
PA (STEP/) STEPHAN J F.  
PA (WATA/) WATANABE C K.  
PA (WILL/) WILLIAMS P M.  
PA (WOOD/) WOOD W I.  
Query Match 45.9%; Score 630.5; DB 5; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 57  
ID ADI17076 standard; protein; 260 AA.  
DE Human NOVX protein homologue SegID 612.  
PN WO200268649-A2.  
PD 06-SEP-2002.  
PA (CURA-) CURAGEN CORP.  
Query Match 45.9%; Score 630.5; DB 5; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 58  
ID ABO17813 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003032156-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 6; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 59  
ID ABO25246 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003050239-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 6; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 60  
ID ABU81067 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003004311-A1.  
PD 02-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 6; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 61  
ID ABU72252 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2002193706-A1.  
PD 19-DEC-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 6; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 62  
ID ADA05702 standard; protein; 260 AA.  
DE Human NOV11h protein SEQ ID NO:62.  
PN WO2003029424-A2.  
PD 10-APR-2003.  
PA (CURA-) CURAGEN CORP.  
Query Match 45.9%; Score 630.5; DB 6; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 63  
ID ABU6767 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003036180-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 6; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 64  
ID ABU84932 standard; protein; 260 AA.  
DE Human secreted and transmembrane PRO polypeptide #8.  
PN US2002177553-A1.  
PD 28-NOV-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 6; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 65  
ID ABU59848 standard; protein; 260 AA.  
DE Novel secreted and transmembrane protein PRO322.  
PN US2003017563-A1.  
PD 23-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 6; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 66  
ID ABU61130 standard; protein; 260 AA.  
DE Human PRO322 polypeptide.  
PN US2002169284-A1.  
PD 14-NOV-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 6; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 67  
ID ABO25038 standard; protein; 260 AA.  
DE Human secreted/transmembrane protein (PRO) #198.  
PN US2003036179-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 6; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 68

ID ABU80399 standard; protein; 260 AA.  
DE Human secreted/transmembrane protein PRO322.  
PN US2003004102-A1.  
PD 02-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 6; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 69  
ID ABU67043 standard; protein; 260 AA.  
DE Human secreted/transmembrane, PRO, protein SEQ ID 396.  
PN US2003032155-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 6; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 70  
ID ADA45915 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003022328-A1.  
PD 30-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 6; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 71  
ID ADA76346 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003073212-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 6; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 72  
ID ADA18996 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003054517-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 6; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 73  
ID ADA61619 standard; protein; 260 AA.  
DE Homo sapiens.  
PN US2003049816-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 6; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 74  
ID ADB27945 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003068796-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 6; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 75  
ID ADB27945 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003082704-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 6; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 76  
ID ADA86424 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003082711-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 6; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 77  
ID ADB15988 standard; protein; 260 AA.

DE Human PRO polypeptide #198.  
PN US2003087350-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 6; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 78  
ID ADA47774 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003073215-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 6; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 79  
ID ADA67569 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003068795-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 6; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 80  
ID ADB30576 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003068794-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 6; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 81  
ID ADA85872 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003082693-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 6; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 82  
ID ADA97084 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003082705-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 6; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 83  
ID ADA79388 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003082763-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 6; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 84  
ID ADA87527 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003087345-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 6; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 85  
ID ADB16729 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003087349-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 6; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 86  
ID ADA91821 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.

PN US2003082694-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 6; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 87  
ID ADB14884 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003087351-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 6; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 88  
ID ADA24934 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003050241-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 6; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 89  
ID ADB18845 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003073211-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 6; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 90  
ID ADA94060 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003077722-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 6; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 91  
ID ADB19956 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003082691-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 6; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 92  
ID ADB13268 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003082710-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 6; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 93  
ID ABO43346 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003044945-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 6; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 94  
ID ABO19701 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003050240-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 6; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 95  
ID ADA12595 standard; protein; 260 AA.  
DE Human secreted/transmembrane polypeptide PRO322.  
PN US2003055216-A1.

PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 6; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 96  
ID ADA74522 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003068798-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 6; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 97  
ID ADB24755 standard; protein; 260 AA.  
DE Human PRO polypeptide SEQ ID NO 396.  
PN US2003077713-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 6; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 98  
ID ADA82279 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003082701-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 6; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 99  
ID ADA75242 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003073216-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 6; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 100  
ID ADA85320 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003082695-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 6; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 101  
ID ADA84768 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003082708-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 6; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 102  
ID ADB30024 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003073214-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 6; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 103  
ID ADA80552 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003082761-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 6; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 104  
ID ADA75794 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003082703-A1.  
PD 01-MAY-2003.

PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 6; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 105  
ID ADA7019 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003073210-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 6; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 106  
ID ADB25315 standard; protein; 260 AA.  
DE Human PRO polypeptide SEQ ID NO 396.  
PN US2003077115-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 6; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 107  
ID ADA93491 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US200307721-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 6; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 108  
ID ADB26841 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003092147-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 6; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 109  
ID ADB31128 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003096386-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 6; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 110  
ID ADA61056 standard; protein; 260 AA.  
DE Homo sapiens.  
PN US2003049817-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 6; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 111  
ID ADB24203 standard; protein; 260 AA.  
DE Human PRO polypeptide SEQ ID NO 396.  
PN US2003077114-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 6; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 112  
ID ADA96532 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003082690-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 6; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 113  
ID ADA81104 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003082702-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.

Query Match 45.9%; Score 630.5; DB 6; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 114  
ID ADA95980 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003082759-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 6; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 115  
ID ADB26289 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003082760-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 6; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 116  
ID ADB21774 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003082765-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 6; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 117  
ID ABO19592 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane polypeptide #60.  
PN US2003049633-A1.  
PD 13-MAR-2003.  
Query Match 45.9%; Score 630.5; DB 6; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 118  
ID ADA77553 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003068797-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 119  
ID ADB18293 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003077110-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 120  
ID ADA86976 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003082709-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 121  
ID ADA88079 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003082700-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 122  
ID ADA46467 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003054516-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;

RESULT 123  
ID ADB28497 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003082699-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 124  
ID ADB29049 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003082706-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 125  
ID ADA77001 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003059509-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 126  
ID ADA88631 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003073213-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 127  
ID ADA97636 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003082686-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 128  
ID ADB27393 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US200302239-A1.  
PD 30-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 129  
ID ADB22326 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003087344-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 130  
ID ADA67017 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003068793-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 131  
ID ADB22878 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US200307711-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 132  
ID ADB23651 standard; protein; 260 AA.  
DE Human PRO polypeptide SEQ ID NO 396.  
PN US2003082764-A1.  
PN US200307712-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 133  
ID ADA92373 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003082712-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 134  
ID ADB15436 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003087352-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 135  
ID ADB38688 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003082766-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 136  
ID ADB38136 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003087347-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 137  
ID ADB66608 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003082689-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 138  
ID ADB89688 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003082698-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 139  
ID ADB90420 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003082762-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 140  
ID ADB80561 standard; protein; 260 AA.  
DE Ovarian cancer-associated protein #63.  
PN WO2002102235-A2.  
PD 27-DEC-2002.  
PA (E0SB-) EOS BIOTECHNOLOGY INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 141  
ID ADB39521 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003082764-A1.



PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 142  
ID ADB73901 standard; protein; 260 AA.  
DE Human PRO polypeptide #60.  
FN US2003045462-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 143  
ID ADB47144 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
FN US2003082687-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 144  
ID ADB86751 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
FN US2003082697-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 145  
ID ADB76617 standard; protein; 260 AA.  
DE Human PRO polypeptide #60.  
FN US2003083248-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 146  
ID ADB77356 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
FN US2003082696-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 147  
ID ADB34513 standard; protein; 260 AA.  
DE Human PRO polypeptide SEQ ID NO 396.  
FN US2003077717-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 148  
ID ADB35617 standard; protein; 260 AA.  
DE Human PRO polypeptide SEQ ID NO 396.  
FN US2003077719-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 149  
ID ADB33961 standard; protein; 260 AA.  
DE Human PRO polypeptide SEQ ID NO 396.  
FN US2003077716-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 150  
ID ADB35065 standard; protein; 260 AA.  
DE Human PRO polypeptide SEQ ID NO 396.  
FN US2003077718-A1.  
PD 24-APR-2003.

PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 151  
ID ADB36169 standard; protein; 260 AA.  
DE Human PRO polypeptide SEQ ID NO 396.  
FN US2003077720-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 152  
ID ADB46564 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
FN US2003082692-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 153  
ID ADC44043 standard; protein; 260 AA.  
DE Human secreted/transmembrane protein, PRO322.  
FN US2003054986-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 154  
ID ADC61803 standard; protein; 260 AA.  
DE Human secreted/transmembrane protein, PRO322.  
FN US2003049684-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 155  
ID ADC63767 standard; protein; 260 AA.  
DE Human secreted/transmembrane protein, PRO322.  
FN US2003054405-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 156  
ID ADC66867 standard; protein; 260 AA.  
DE Human secreted/transmembrane protein, PRO322.  
FN US2003060406-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 157  
ID ADC68991 standard; protein; 260 AA.  
DE Human secreted/transmembrane protein, PRO322.  
FN US2003064407-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 158  
ID ADC63051 standard; protein; 260 AA.  
DE Human secreted/transmembrane protein, PRO322.  
FN US2003069648-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 159  
ID ADC68116 standard; protein; 260 AA.  
DE Human secreted/transmembrane protein, PRO322.  
FN US2003069178-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.

Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 160  
ID ADC41436 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein, PRO322.  
PN US2003072745-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 161  
ID ADC67491 standard; protein; 260 AA.  
DE Human secreted/transmembrane protein, PRO322.  
PN US2003073131-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 162  
ID ADC62427 standard; protein; 260 AA.  
DE Human secreted/transmembrane protein, PRO322.  
PN US2003073624-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 163  
ID ADC42060 standard; protein; 260 AA.  
DE Human secreted/transmembrane protein, PRO322.  
PN US2003104998-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 164  
ID ADC50437 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003092106-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 165  
ID ADC71984 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003092107-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 166  
ID ADC52970 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003092105-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 167  
ID ADC52970 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein Seq ID396.  
PN US2003087365-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 168  
ID ADC57324 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein Seq ID396.  
PN US2003087366-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 169  
ID ADC60515 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003087367-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 170  
ID ADC50990 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003087361-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 171  
ID ADC65517 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003087362-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 172  
ID ADC54615 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein Seq ID396.  
PN US2003087363-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 173  
ID ADC53576 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein Seq ID396.  
PN US2003087364-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 174  
ID ADC59099 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein Seq ID396.  
PN US2003087359-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 175  
ID ADC55977 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein Seq ID396.  
PN US2003087360-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 176  
ID ADC58547 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein Seq ID396.  
PN US2003087346-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 177  
ID ADD03221 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003092104-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;

RESULT 178  
ID ADC90213 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003087348-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 179  
ID ADC69632 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003194770-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 180  
ID ADC48521 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003194773-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 181  
ID ADP10050 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003194776-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 182  
ID ADD04625 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003087354-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 183  
ID ADC80581 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003092103-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 184  
ID ADD09100 standard; protein; 260 AA.  
DE Human kallikrein 8 protein SEQ ID NO:2.  
PN WO2003085404-A1.  
PD 16-OCT-2003.  
PA (MOUN ) MOUNT SINAI HOSPITAL.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 185  
ID ADD11088 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003194774-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 186  
ID ADD10361 standard; protein; 260 AA.  
DE Human secreted/transmembrane PRO polypeptide #36.  
PN US2003105011-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 187

ID ADC47969 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003194771-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 188  
ID ADC80029 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003087358-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 189  
ID ADD11321 standard; protein; 260 AA.  
DE Human secreted/transmembrane PRO polypeptide #36.  
PN US2003105013-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 190  
ID ADD09498 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003194775-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 191  
ID ADD41211 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003203438-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 192  
ID ADD52350 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003194769-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 193  
ID ADD53090 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003194792-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 194  
ID ADD53642 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003203437-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 195  
ID ADD37114 standard; protein; 260 AA.  
DE Human secreted/transmembrane PRO polypeptide #36.  
PN US2003105012-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 196  
ID ABW00074 standard; protein; 260 AA.

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DE Human tumour antigen derived gene-14 (TAGD-14) protein.  
 PN US2002037581-A1.  
 PD 28-MAR-2002.  
 PA (QABR-) DAB RES FOUND.  
 Query Match 45.9%; Score 630.5; DB 7; Length 260;  
 Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
 RESULT 197  
 ID ADD51798 standard; protein; 260 AA.  
 DE Human PRO polypeptide #198.  
 PN US2003194779-A1.  
 PD 16-OCT-2003.  
 PA (GETH) GENENTECH INC.  
 Query Match 45.9%; Score 630.5; DB 7; Length 260;  
 Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
 RESULT 198  
 ID ADD02597 standard; protein; 260 AA.  
 DE Human PRO polypeptide #198.  
 PN US2003203431-A1.  
 PD 30-OCT-2003.  
 PA (GETH) GENENTECH INC.  
 Query Match 45.9%; Score 630.5; DB 7; Length 260;  
 Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
 RESULT 199  
 ID ADD02031 standard; protein; 260 AA.  
 DE Human PRO polypeptide #198.  
 PN US2003203430-A1.  
 PD 30-OCT-2003.  
 PA (GETH) GENENTECH INC.  
 Query Match 45.9%; Score 630.5; DB 7; Length 260;  
 Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
 RESULT 200  
 ID ADD54213 standard; protein; 260 AA.  
 DE Novel human secreted and transmembrane protein PRO322.  
 PN US2003203432-A1.  
 PD 30-OCT-2003.  
 PA (GETH) GENENTECH INC.  
 Query Match 45.9%; Score 630.5; DB 7; Length 260;  
 Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
 RESULT 201  
 ID ADE49429 standard; protein; 260 AA.  
 DE Human secreted/transmembrane protein, PRO322.  
 PN US2003096744-A1.  
 PD 22-MAY-2003.  
 PA (GETH) GENENTECH INC.  
 Query Match 45.9%; Score 630.5; DB 7; Length 260;  
 Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
 RESULT 202  
 ID ADD92530 standard; protein; 260 AA.  
 DE Human PRO polypeptide #198.  
 PN US2003199030-A1.  
 PD 23-OCT-2003.  
 PA (GETH) GENENTECH INC.  
 Query Match 45.9%; Score 630.5; DB 7; Length 260;  
 Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
 RESULT 203  
 ID ADD91426 standard; protein; 260 AA.  
 DE Human PRO polypeptide #198.  
 PN US2003199055-A1.  
 PD 23-OCT-2003.  
 PA (GETH) GENENTECH INC.  
 Query Match 45.9%; Score 630.5; DB 7; Length 260;  
 Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
 RESULT 204  
 ID ADE04040 standard; protein; 260 AA.  
 DE Human PRO polypeptide #198.  
 PN US2003199057-A1.  
 PD 23-OCT-2003.  
 PA (GETH) GENENTECH INC.  
 Query Match 45.9%; Score 630.5; DB 7; Length 260;  
 Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
 RESULT 205  
 ID ADE32337 standard; protein; 260 AA.  
 DE Novel human secreted and transmembrane protein PRO322.

PN US2003194765-A1.  
 PD 16-OCT-2003.  
 PA (GETH) GENENTECH INC.  
 Query Match 45.9%; Score 630.5; DB 7; Length 260;  
 Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
 RESULT 206  
 ID ADE22269 standard; protein; 260 AA.  
 DE Human PRO polypeptide #198.  
 PN US2003199056-A1.  
 PD 23-OCT-2003.  
 PA (GETH) GENENTECH INC.  
 Query Match 45.9%; Score 630.5; DB 7; Length 260;  
 Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
 RESULT 207  
 ID ADD79493 standard; protein; 260 AA.  
 DE Human PRO polypeptide #198.  
 PN US2003203428-A1.  
 PD 30-OCT-2003.  
 PA (GETH) GENENTECH INC.  
 Query Match 45.9%; Score 630.5; DB 7; Length 260;  
 Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
 RESULT 208  
 ID ADE35483 standard; protein; 260 AA.  
 DE Human secreted/transmembrane protein, PRO322.  
 PN US2003203434-A1.  
 PD 30-OCT-2003.  
 PA (GETH) GENENTECH INC.  
 Query Match 45.9%; Score 630.5; DB 7; Length 260;  
 Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
 RESULT 209  
 ID ADE16597 standard; protein; 260 AA.  
 DE Human secreted/transmembrane protein, PRO322.  
 PN US2003203435-A1.  
 PD 30-OCT-2003.  
 PA (GETH) GENENTECH INC.  
 Query Match 45.9%; Score 630.5; DB 7; Length 260;  
 Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
 RESULT 210  
 ID ADD73212 standard; protein; 260 AA.  
 DE Human secreted/transmembrane protein, PRO322.  
 PN US2003203436-A1.  
 PD 30-OCT-2003.  
 PA (GETH) GENENTECH INC.  
 Query Match 45.9%; Score 630.5; DB 7; Length 260;  
 Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
 RESULT 211  
 ID ADE42029 standard; protein; 260 AA.  
 DE Human PRO polypeptide #198.  
 PN US2003194772-A1.  
 PD 16-OCT-2003.  
 PA (GETH) GENENTECH INC.  
 Query Match 45.9%; Score 630.5; DB 7; Length 260;  
 Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
 RESULT 212  
 ID ADE17846 standard; protein; 260 AA.  
 DE Human PRO polypeptide #198.  
 PN US2003199023-A1.  
 PD 23-OCT-2003.  
 PA (GETH) GENENTECH INC.  
 Query Match 45.9%; Score 630.5; DB 7; Length 260;  
 Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
 RESULT 213  
 ID ADD91978 standard; protein; 260 AA.  
 DE Human PRO polypeptide #198.  
 PN US2003199053-A1.  
 PD 23-OCT-2003.  
 PA (GETH) GENENTECH INC.  
 Query Match 45.9%; Score 630.5; DB 7; Length 260;  
 Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
 RESULT 214  
 ID ADE33441 standard; protein; 260 AA.  
 DE Novel human secreted and transmembrane protein PRO322.  
 PN US2003194767-A1.

PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 215  
ID ADE33993 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003194791-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 216  
ID ADE00045 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003207417-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 217  
ID ADD93082 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003194768-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 218  
ID ADE172570 standard; protein; 260 AA.  
DE Human secreted/transmembrane protein, PRO322.  
PN US2003194781-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 219  
ID ADE19502 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003199025-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 220  
ID ADE18950 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003199026-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 221  
ID ADE43146 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003199033-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 222  
ID ADD95935 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003199059-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 223  
ID ADE22821 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003199064-A1.  
PD 23-OCT-2003.

PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 224  
ID ADE78939 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003203429-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 225  
ID ADE32889 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003194766-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 226  
ID ADE42581 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003199032-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 227  
ID ADE17221 standard; protein; 260 AA.  
DE Human secreted/transmembrane protein, PRO322.  
PN US2003203433-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 228  
ID ADD80597 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003207418-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 229  
ID ADD89625 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003199028-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 230  
ID ADE40909 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003199031-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 231  
ID ADE04708 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003199034-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 232  
ID ADE92837 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003194777-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.

Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 233  
ID ADF47235 standard; protein; 260 AA.  
DE Human secreted/transmembrane protein, PRO322.  
PN US2003195333-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 234  
ID ADG21546 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003207355-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 235  
ID ADG23187 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003207384-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 236  
ID ADF97522 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003207370-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 237  
ID ADG80896 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003207373-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 238  
ID ADG52992 standard; protein; 260 AA.  
DE Human secreted/transmembrane protein, PRO322.  
PN US2003216561-A1.  
PD 20-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 239  
ID ADG60312 standard; protein; 260 AA.  
DE Human secreted/transmembrane protein, PRO322.  
PN US2003206915-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 240  
ID ADG80034 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003207372-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 241  
ID ADH55326 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003207381-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;

Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 242  
ID ADH5878 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003207379-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 243  
ID ADI61072 standard; protein; 260 AA.  
DE Human secreted/transmembrane protein, PRO322.  
PN US2003077700-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 244  
ID ADI64097 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003207385-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 245  
ID ADH81959 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003207388-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 246  
ID ADH81407 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003207377-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 247  
ID ADM82576 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003087355-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 248  
ID ADN15975 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003087353-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 249  
ID ADN16604 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003087385-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 250  
ID ADN39182 standard; protein; 260 AA.  
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:500.  
PN WO2003042661-A2.  
PD 22-MAY-2003.  
PA (EOSB-) EOS BIOTECHNOLOGY INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;

RESULT 251  
ID ADN15423 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003087356-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 252  
ID ADN14871 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003087357-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 253  
ID ADI65046 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003207386-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 254  
ID ADI63545 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003207387-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 255  
ID ADC81133 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003092115-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 256  
ID ADD76581 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003100087-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 257  
ID ADD87945 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003092113-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 258  
ID ADD86349 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003203440-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 259  
ID ADS75797 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003211571-A1.  
PD 13-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 260

ID ADE48729 standard; protein; 260 AA.  
DE Human secreted/transmembrane protein, PRO322.  
PN US2003104536-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 261  
ID ADE41322 standard; protein; 260 AA.  
DE Human secreted/transmembrane PRO polypeptide #36.  
PN US2003100497-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 262  
ID ADE23373 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003092108-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 263  
ID ADE23925 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003092110-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 264  
ID ADE24568 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003092111-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 265  
ID ADE87393 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003203439-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 266  
ID ADE89259 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003199062-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 267  
ID ADE18398 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003194794-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 268  
ID ADE88707 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003199054-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 269  
ID ADE89830 standard; protein; 260 AA.

DE Human secreted/transmembrane protein, PRO322.  
PN US2003130181-A1.  
PD 10-JUL-2003.  
PA (ASHK/) ASHKENAZI A J.  
PA (BAKE/) BAKER K P.  
PA (BOTS/) BOTSTEIN D.  
PA (DESN/) DESNOYERS L.  
PA (EATO/) EATON D L.  
PA (FERR/) FERRARA N.  
PA (FILV/) FILVAROFF E.  
PA (FONG/) FONG S.  
PA (GAOW/) GAO W.  
PA (GERB/) GERBER H.  
PA (GERR/) GERRITSEN M E.  
PA (GODD/) GODDARD A.  
PA (GODO/) GODOWSKI P J.  
PA (GIRM/) GIRMALDI J C.  
PA (GURN/) GURNEY A L.  
PA (HILL/) HILLAN K J.  
PA (KLJA/) KLJAVIN I J.  
PA (KUOS/) KUO S S.  
PA (NAPI/) NAPIER M A.  
PA (PANG/) PAN J.  
PA (PAON/) PAONI N F.  
PA (ROYM/) ROY M A.  
PA (SHEL/) SHELTON D L.  
PA (STEW/) STEWART T A.  
PA (TUMA/) TUMAS D.  
PA (WILL/) WILLIAMS P M.  
PA (WOOD/) WOOD W I.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 270  
ID ADF61470 standard; protein; 260 AA.  
DE Human secreted/transmembrane protein, PRO322.  
PN US2003195345-A1.  
PD 16-OCT-2003.  
PA (GPTH/) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 271  
ID ADF40162 standard; protein; 260 AA.  
DE Human secreted/transmembrane protein, PRO322.  
PN US2003198994-A1.  
PD 23-OCT-2003.  
PA (GPTH/) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 272  
ID ADF45958 standard; protein; 260 AA.  
DE Human secreted/transmembrane protein, PRO322.  
PN US2003195148-A1.  
PD 16-OCT-2003.  
PA (GPTH/) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 273  
ID ADF94727 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003199027-A1.  
PD 23-OCT-2003.  
PA (GPTH/) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 274  
ID ADE91138 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003199061-A1.  
PD 23-OCT-2003.  
PA (GPTH/) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 275  
ID ADE92285 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003199052-A1.  
PD 23-OCT-2003.  
PA (GPTH/) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 276  
ID ADE93389 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003199060-A1.  
PD 23-OCT-2003.  
PA (GPTH/) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 277  
ID ADF24354 standard; protein; 260 AA.  
DE Human secreted/transmembrane protein, PRO322.  
PN US2003204055-A1.  
PD 30-OCT-2003.  
PA (GPTH/) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 278  
ID ADF40786 standard; protein; 260 AA.  
DE Human secreted/transmembrane protein, PRO322.  
PN US2003199021-A1.  
PD 23-OCT-2003.  
PA (GPTH/) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 279  
ID ADF23730 standard; protein; 260 AA.  
DE Human secreted/transmembrane protein, PRO322.  
PN US2003203402-A1.  
PD 30-OCT-2003.  
PA (GPTH/) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 280  
ID ADF33713 standard; protein; 260 AA.  
DE Human secreted/transmembrane protein, PRO322.  
PN US2003194780-A1.  
PD 16-OCT-2003.  
PA (GPTH/) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 281  
ID ADF34970 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003199029-A1.  
PD 23-OCT-2003.  
PA (GPTH/) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 282  
ID ADF27180 standard; protein; 260 AA.  
DE Human secreted/transmembrane protein, PRO322.  
PN US2003199436-A1.  
PD 23-OCT-2003.  
PA (GPTH/) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 283  
ID ADF27816 standard; protein; 260 AA.  
DE Human secreted/transmembrane protein, PRO322.  
PN US2003199437-A1.  
PD 23-OCT-2003.  
PA (GPTH/) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 284  
ID ADE92285 standard; protein; 260 AA.



DE Novel human secreted and transmembrane protein PRO322.  
PN US2003199051-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 285  
ID ADE90586 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003199063-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 286  
ID ADF41410 standard; protein; 260 AA.  
DE Human secreted/transmembrane protein, PRO322.  
PN US2003199435-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 287  
ID ADF33089 standard; protein; 260 AA.  
DE Human secreted/transmembrane protein, PRO322.  
PN US2003211091-A1.  
PD 13-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 288  
ID ADF25455 standard; protein; 260 AA.  
DE Human secreted/transmembrane protein, PRO322.  
PN US2003211092-A1.  
PD 13-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 289  
ID ADF26556 standard; protein; 260 AA.  
DE Human secreted/transmembrane protein, PRO322.  
PN US2003199674-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 290  
ID ADF34345 standard; protein; 260 AA.  
DE Human secreted/transmembrane protein, PRO322.  
PN US2003194410-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 291  
ID ADF46582 standard; protein; 260 AA.  
DE Human secreted/transmembrane protein, PRO322.  
PN US2003195344-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 292  
ID ADF91733 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003199058-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 293  
ID ADG02312 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.

PN US2003207352-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 294  
ID ADG22098 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003207360-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 295  
ID ADG20168 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003207376-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 296  
ID ADF98074 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003207422-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 297  
ID ADG24291 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003207426-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 298  
ID ADF98645 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003208055-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 299  
ID ADG03476 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003207351-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 300  
ID ADF99197 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003207353-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 301  
ID ADG16782 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003207359-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 302  
ID ADG05241 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003207375-A1.

PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 303  
ID ADG19508 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003207425-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 304  
ID ADG13345 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003207357-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 305  
ID ADG08402 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003207424-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 306  
ID ADG15572 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003219885-A1.  
PD 27-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 307  
ID ADG96970 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003207371-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 308  
ID ADG06155 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003207374-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 309  
ID ADG23739 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003207389-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 310  
ID ADG04028 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003207423-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 311  
ID ADG24929 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003207427-A1.  
PD 06-NOV-2003.

PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 312  
ID ADG07226 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003207350-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 313  
ID ADG07778 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003207356-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 314  
ID ADG55273 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003194778-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 315  
ID ADG60937 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003207390-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 316  
ID ADG62041 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003207428-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 317  
ID ADG82242 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003207358-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 318  
ID ADG57481 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003207362-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 319  
ID ADG56929 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003207364-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 320  
ID ADG55825 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003207365-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;

Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 321  
ID ADG58585 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003207368-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 322  
ID ADG70951 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003207420-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 323  
ID ADG58033 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003207363-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 324  
ID ADG53617 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003207415-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 325  
ID ADG71503 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003207421-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 326  
ID ADG50568 standard; protein; 260 AA.  
DE Human secreted/transmembrane protein, PRO322.  
PN US2003207803-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 327  
ID ADG81690 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003207805-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 328  
ID ADH30652 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003077723-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 329  
ID ADH12019 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003207419-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;

RESULT 330  
ID ADG49944 standard; protein; 260 AA.  
DE Human secreted/transmembrane protein, PRO322.  
PN US2003215905-A1.  
PD 20-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 331  
ID ADG51816 standard; protein; 260 AA.  
DE Human secreted/transmembrane protein, PRO322.  
PN US2003215908-A1.  
PD 20-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 332  
ID ADG52441 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003207414-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 333  
ID ADG54169 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003207416-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 334  
ID ADG49320 standard; protein; 260 AA.  
DE Human secreted/transmembrane protein, PRO322.  
PN US2003216305-A1.  
PD 20-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 335  
ID ADG81138 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003194793-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 336  
ID ADG56377 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003207366-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 337  
ID ADH12643 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003207378-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 338  
ID ADG48696 standard; protein; 260 AA.  
DE Human secreted/transmembrane protein, PRO322.  
PN US2003216560-A1.  
PD 20-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 339  
ID ADH12019 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003207419-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;

ID ADG61489 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003207429-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 340  
ID ADH28576 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US200302231-A1.  
PD 30-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 341  
ID ADG54721 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003207367-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 342  
ID ADG59761 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003207369-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 343  
ID ADG51192 standard; protein; 260 AA.  
DE Human secreted/transmembrane protein, PRO322.  
PN US2004005312-A1.  
PD 08-JAN-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 344  
ID ADH43505 standard; protein; 260 AA.  
DE Human PRO polypeptide #36.  
PN US2003224984-A1.  
PD 04-DEC-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 345  
ID ADG59136 standard; protein; 260 AA.  
DE Human secreted/transmembrane protein, PRO322.  
PN US2004005657-A1.  
PD 08-JAN-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 346  
ID ADG62592 standard; protein; 260 AA.  
DE Human secreted/transmembrane protein, PRO322.  
PN US2004006219-A1.  
PD 08-JAN-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 347  
ID ADH18185 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003207361-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 348  
ID ADI39730 standard; protein; 260 AA.

DE Human TAGD-14 protein.  
PN US6642013-B1.  
PD 04-NOV-2003.  
PA (UYAR-) UNIV ARKANSAS MEDICAL SCI.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 349  
ID ADH25617 standard; protein; 260 AA.  
DE Human neurotrophin homologue related protein sequence SEQ ID NO:395.  
PN EPI386931-A1.  
PD 04-FEB-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 350  
ID ADG0928 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2004009548-A1.  
PD 15-JAN-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 351  
ID ADI15399 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003207382-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 352  
ID ADG09276 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2004009547-A1.  
PD 15-JAN-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 353  
ID ADI14731 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003207383-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 354  
ID ADI18326 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003207349-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 355  
ID ADI37154 standard; protein; 260 AA.  
DE Human TAGD-14 protein.  
PN US2003199010-A1.  
PD 23-OCT-2003.  
PA (UYAR-) UNIV ARKANSAS.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 356  
ID ADG63607 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2004039164-A1.  
PD 26-FEB-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 357  
ID ADJ77502 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.

PN US2004038336-A1.  
 PD 26-FEB-2004.  
 PA (GETH ) GENENTECH INC.  
 Query Match 45.9%; Score 630.5; DB 8; Length 260;  
 Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
 RESULT 358  
 ID ADR82B50 standard; protein; 260 AA.  
 DE Human PRO polypeptide #36.  
 PN US2004043927-A1.  
 PD 04-MAR-2004.  
 PA (GETH ) GENENTECH INC.  
 Query Match 45.9%; Score 630.5; DB 8; Length 260;  
 Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
 RESULT 359  
 ID ADJ65624 standard; protein; 260 AA.  
 DE Human PRO polypeptide #198.  
 PN US2004038335-A1.  
 PD 26-FEB-2004.  
 PA (GETH ) GENENTECH INC.  
 Query Match 45.9%; Score 630.5; DB 8; Length 260;  
 Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
 RESULT 360  
 ID ADM27760 standard; protein; 260 AA.  
 DE Human PRO polypeptide #198.  
 PN US2004048333-A1.  
 PD 11-MAR-2004.  
 PA (GETH ) GENENTECH INC.  
 Query Match 45.9%; Score 630.5; DB 8; Length 260;  
 Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
 RESULT 361  
 ID ADM17394 standard; protein; 260 AA.  
 DE Human secreted/transmembrane protein, PRO322.  
 PN US2004048332-A1.  
 PD 11-MAR-2004.  
 PA (GETH ) GENENTECH INC.  
 Query Match 45.9%; Score 630.5; DB 8; Length 260;  
 Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
 RESULT 362  
 ID ADI07228 standard; protein; 260 AA.  
 DE Human secreted/transmembrane protein, PRO322.  
 PN US2004063921-A1.  
 PD 01-APR-2004.  
 PA (GETH ) GENENTECH INC.  
 Query Match 45.9%; Score 630.5; DB 8; Length 260;  
 Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
 RESULT 363  
 ID ADM42484 standard; protein; 260 AA.  
 DE Human PRO polypeptide #198.  
 PN US2004058424-A1.  
 PD 25-MAR-2004.  
 PA (GETH ) GENENTECH INC.  
 Query Match 45.9%; Score 630.5; DB 8; Length 260;  
 Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
 RESULT 364  
 ID ADM62866 standard; protein; 260 AA.  
 DE Human NOV11h.  
 PN US2004038223-A1.  
 PD 26-FEB-2004.  
 PA (SMIT ) SMITHSON G.  
 PA (MILL ) MILLET I.  
 PA (PEYM ) PEYMAN J A.  
 PA (KEKU ) KEKUDA R.  
 PA (JUJJ ) JU J.  
 PA (LILL ) LI L.  
 PA (GUOX ) GUO X.  
 PA (PATI ) PATTURAJAN M.  
 PA (SPYT ) SPYTEK K A.  
 PA (EDIN ) EDINGER S R.  
 PA (ELLE ) ELLERMAN K.  
 PA (NALY ) MALYANKAR U M.  
 PA (ORTT ) ORT T.  
 PA (GORM ) GORMAN L.  
 PA (ZERH ) ZERHUSEN B D.

PA (ANDE ) ANDERSON D W.  
 PA (ZHON ) ZHONG M.  
 PA (CATT ) CATTERTON E.  
 PA (JIWW ) JI W.  
 PA (MILL ) MILLER C E.  
 PA (RASI ) RASTELLI L.  
 PA (STON ) STONE D J.  
 PA (PENA ) PENA C E A.  
 PA (SHEN ) SHENOY S G.  
 PA (SHIM ) SHIMKETS R A.  
 PA (ROTH ) ROTHENBERG M E.  
 PA (LEAC ) LEACH M D.  
 PA (AGEE ) AGEE M L.  
 PA (BERG ) BERGHS C.  
 PA (DIPI ) DIPIPO V A.  
 PA (EISE ) EISEN A.  
 PA (GANG ) GANGOLLI E A.  
 PA (RIEG ) RIEGER D K.  
 PA (SPAD ) SPADERNA S K.  
 Query Match 45.9%; Score 630.5; DB 8; Length 260;  
 Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
 RESULT 365  
 ID ADN04214 standard; protein; 260 AA.  
 DE Antiprosclerotic protein sequence #302.  
 PN WO2004028479-A2.  
 PD 08-APR-2004.  
 PA (GETH ) GENENTECH INC.  
 Query Match 45.9%; Score 630.5; DB 8; Length 260;  
 Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
 RESULT 366  
 ID ADM28346 standard; protein; 260 AA.  
 DE Human PRO polypeptide #198.  
 PN US2004077064-A1.  
 PD 22-APR-2004.  
 PA (GETH ) GENENTECH INC.  
 Query Match 45.9%; Score 630.5; DB 8; Length 260;  
 Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
 RESULT 367  
 ID ADI95828 standard; protein; 260 AA.  
 DE Human PRO polypeptide #198.  
 PN US2003077659-A1.  
 PD 24-APR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 45.9%; Score 630.5; DB 8; Length 260;  
 Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
 RESULT 368  
 ID ADI96380 standard; protein; 260 AA.  
 DE Novel human secreted and transmembrane protein PRO322.  
 PN US2003207354-A1.  
 PD 06-NOV-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 45.9%; Score 630.5; DB 8; Length 260;  
 Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
 RESULT 369  
 ID ADR72883 standard; protein; 260 AA.  
 DE Human ovarian cancer-related tumour marker kallikrein 8 (hK8) protein.  
 PN WO2004075713-A2.  
 PD 10-SEP-2004.  
 PA (MOUN ) MOUNT SINAI HOSPITAL.  
 Query Match 45.9%; Score 630.5; DB 8; Length 260;  
 Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
 RESULT 370  
 ID AAY32853 standard; protein; 305 AA.  
 DE Human serine protease protein sequence.  
 PN JP1125765-A.  
 PD 24-AUG-1999.  
 PA (SUNR ) SUNTORY LTD.  
 Query Match 45.6%; Score 627; DB 2; Length 305;  
 Best Local Similarity 50.9%; Pred. No. 2.4e-40;  
 RESULT 371  
 ID AAB37985 standard; protein; 306 AA.  
 DE Human secreted protein encoded by gene 2 clone HWJAE49.  
 PN WO200055371-A1.

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PD 21-SEP-2000.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 45.3%; Score 627; DB 3; Length 306;  
Best Local Similarity 50.9%; Pred. No. 2.4e-40;  
RESULT 372  
ID ABP41332 standard; protein; 315 AA.  
DE Human ovarian antigen HCOQP78, SEQ ID NO:2464.  
PN WO200200677-A1.  
PD 03-JAN-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 45.6%; Score 627; DB 5; Length 315;  
Best Local Similarity 50.9%; Pred. No. 2.4e-40;  
RESULT 373  
ID AAW87703 standard; protein; 260 AA.  
DE A human serine protease designated HGBAB90.  
PN EP887414-A2.  
PD 30-DEC-1998.  
PA (SNIK-) SMITHKLINE BEECHAM PLC.  
Query Match 45.6%; Score 626.5; DB 2; Length 260;  
Best Local Similarity 50.4%; Pred. No. 2.2e-40;  
RESULT 374  
ID AAB21311 standard; protein; 275 AA.  
DE Human neuropsin.  
PN WO2000053776-A2.  
PD 14-SEP-2000.  
PA (MOUN-) MOUNT SINAI HOSPITAL.  
Query Match 45.6%; Score 626.5; DB 3; Length 275;  
Best Local Similarity 50.4%; Pred. No. 2.3e-40;  
RESULT 375  
ID AAW10694 standard; protein; 260 AA.  
DE Human recombinant neuropsin, used for antibody production.  
PN JP08245700-A.  
PD 24-SEP-1996.  
PA (IGAK-) IGAKU SEIBUTSUGAKU KENKYUSHO KK.  
Query Match 45.3%; Score 622.5; DB 2; Length 260;  
Best Local Similarity 49.0%; Pred. No. 4.5e-40;  
RESULT 376  
ID AAW12393 standard; protein; 260 AA.  
DE Mouse neuropsin protein.  
PN JP08311099-A.  
PD 26-NOV-1996.  
PA (SHIO/) SHIOZAKA S.  
Query Match 45.3%; Score 622.5; DB 2; Length 260;  
Best Local Similarity 49.0%; Pred. No. 4.5e-40;  
RESULT 377  
ID AAY06438 standard; protein; 260 AA.  
DE Human protease HUPM-7.  
PN WO9936550-A2.  
PD 22-JUL-1999.  
PA (INCY-) INCYTE PHARM INC.  
Query Match 45.3%; Score 622.5; DB 2; Length 260;  
Best Local Similarity 49.8%; Pred. No. 4.5e-40;  
RESULT 378  
ID ABB57219 standard; protein; 260 AA.  
DE Mouse ischaemic condition related protein sequence SEQ ID NO:533.  
PN WO200188188-A2.  
PD 22-NOV-2001.  
PA (UYNI-) UNIV NIHON SCHOOL JURIDICAL PERSON.  
Query Match 45.3%; Score 622.5; DB 5; Length 260;  
Best Local Similarity 49.0%; Pred. No. 4.5e-40;  
RESULT 379  
ID ADI17073 standard; protein; 260 AA.  
DE Murine NOVX protein homologue SeqID 609.  
PN WO200268649-A2.  
PD 06-SEP-2002.  
PA (CURA-) CURAGEN CORP.  
Query Match 45.3%; Score 622.5; DB 5; Length 260;  
Best Local Similarity 49.0%; Pred. No. 4.5e-40;  
RESULT 380  
ID ADI39731 standard; protein; 260 AA.  
DE Mouse neuropsin protein.  
PN US6642013-B1.  
PD 04-NOV-2003.

PA (UYAR-) UNIV ARKANSAS MEDICAL SCI.  
Query Match 45.3%; Score 622.5; DB 8; Length 260;  
Best Local Similarity 49.0%; Pred. No. 4.5e-40;  
RESULT 381  
ID ADI37155 standard; protein; 260 AA.  
DE Mouse neuropsin.  
PN US2003199010-A1.  
PD 23-OCT-2003.  
PA (UYAR-) UNIV ARKANSAS.  
Query Match 45.3%; Score 622.5; DB 8; Length 260;  
Best Local Similarity 49.0%; Pred. No. 4.5e-40;  
RESULT 382  
ID ADI17074 standard; protein; 260 AA.  
DE Rat NOVX protein homologue SeqID 610.  
PN WO200268649-A2.  
PD 06-SEP-2002.  
PA (CURA-) CURAGEN CORP.  
Query Match 45.2%; Score 621.5; DB 5; Length 260;  
Best Local Similarity 48.6%; Pred. No. 5.3e-40;  
RESULT 383  
ID AAB21325 standard; protein; 250 AA.  
DE Human TLSP.  
PN WO2000053776-A2.  
PD 14-SEP-2000.  
PA (MOUN-) MOUNT SINAI HOSPITAL.  
Query Match 45.0%; Score 618.5; DB 3; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 384  
ID AAY99390 standard; protein; 250 AA.  
DE Human PRO1279 (UNQ649) amino acid sequence SEQ ID NO:170.  
PN WO200012708-A2.  
PD 09-MAR-2000.  
PA (GETH-) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 3; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 385  
ID AAB66139 standard; protein; 250 AA.  
DE Protein of the invention #51.  
PN WO200078961-A1.  
PD 28-DEC-2000.  
PA (GETH-) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 4; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 386  
ID AAU12424 standard; protein; 250 AA.  
DE Human PRO1279 polypeptide sequence.  
PN WO200140466-A2.  
PD 07-JUN-2001.  
PA (GETH-) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 4; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 387  
ID ABB50479 standard; protein; 250 AA.  
DE Human secreted protein encoded by gene 179 SEQ ID NO:427.  
PN WO200162891-A2.  
PD 30-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 45.0%; Score 618.5; DB 4; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 388  
ID AAU83684 standard; protein; 250 AA.  
DE Human PRO protein, Seq ID No 186.  
PN WO200208288-A2.  
PD 31-JAN-2002.  
PA (GETH-) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 5; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 389  
ID ABG61816 standard; protein; 250 AA.  
DE Prostate cancer-associated protein #17.  
PN WO200230268-A2.  
PD 18-APR-2002.  
PA (EOSB-) EOS BIOTECHNOLOGY INC.

Query Match 45.0%; Score 618.5; DB 5; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 390  
ID ABB84920 standard; protein; 250 AA.  
DE Human PRO1279 protein sequence SEQ ID NO:208.  
PN WO200200690-A2.  
PD 03-JAN-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 5; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 391  
ID ABB95526 standard; protein; 250 AA.  
DE Human angio genesis related protein PRO1279 SEQ ID NO: 208.  
PN WO200208284-A2.  
PD 31-JAN-2002.  
PA (GETH ) GENENTECH INC.  
PA (BAKE/) BAKER K P.  
PA (FERR/) FERRARA N.  
PA (GERB/) GERBER H.  
PA (GERR/) GERRITSEN M E.  
PA (GODD/) GODDARD A.  
PA (GODO/) GODOWSKI P J.  
PA (GURN/) GURNEY A L.  
PA (HILL/) HILLAN K J.  
PA (MARS/) MARSTERS S A.  
PA (PANJ/) PAN J.  
PA (PAON/) PAONI N F.  
PA (STEP/) STEPHAN J F.  
PA (WATA/) WATANABE C K.  
PA (WILL/) WILLIAMS P M.  
PA (WOOD/) WOOD W I.  
Query Match 45.0%; Score 618.5; DB 5; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 392  
ID ABO17868 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003032156-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 6; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 393  
ID ABU80831 standard; protein; 250 AA.  
DE Human PRO polypeptide #93.  
PN US2003036635-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 6; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 394  
ID ABO33797 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003045687-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 6; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 395  
ID ASU81122 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003004311-A1.  
PD 02-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 6; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 396  
ID ABU56739 standard; protein; 250 AA.  
DE Lung cancer-associated polypeptide #332.  
PN WO200286443-A2.  
PD 31-OCT-2002.  
PA (EOSB-) EOS BIOTECHNOLOGY INC.  
Query Match 45.0%; Score 618.5; DB 6; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 397  
ID ABU66822 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003036180-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 6; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 398  
ID ABU59903 standard; protein; 250 AA.  
DE Novel secreted and transmembrane protein PRO1279.  
PN US2003017563-A1.  
PD 23-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 6; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 399  
ID ABO25093 standard; protein; 250 AA.  
DE Human secreted/transmembrane protein (PRO) #253.  
PN US2003036179-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 6; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 400  
ID ABU82140 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003088063-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 6; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 401  
ID ABU67098 standard; protein; 250 AA.  
DE Human secreted/transmembrane, PRO, protein SEQ ID 506.  
PN US2003032155-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 6; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 402  
ID ADA46025 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003022328-A1.  
PD 30-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 6; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 403  
ID ADA76456 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003073212-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 6; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 404  
ID ABJ72320 standard; protein; 250 AA.  
DE Human PRO1279 protein.  
PN US2003050448-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 6; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 405  
ID ADA19106 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003054517-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 6; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 406  
ID ABO56739 standard; protein; 250 AA.  
DE Lung cancer-associated polypeptide #332.  
PN WO200286443-A2.  
PD 31-OCT-2002.  
PA (EOSB-) EOS BIOTECHNOLOGY INC.  
Query Match 45.0%; Score 618.5; DB 6; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;

ID ADA61729 standard; protein; 250 AA.  
DE Homo sapiens.  
PN US2003049816-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 6; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 407  
ID ADB19514 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003068796-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 6; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 408  
ID ADB28055 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003082704-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 6; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 410  
ID ADA86534 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003082711-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 6; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 411  
ID ADA47884 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003073215-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 6; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 412  
ID ABO44736 standard; protein; 250 AA.  
DE Novel human secreted protein #179.  
PN US2003065160-A1.  
PD 03-APR-2003.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 45.0%; Score 618.5; DB 6; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 413  
ID ABO33632 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003073130-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 6; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 414  
ID ADA67679 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003068795-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 6; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 415  
ID ADB30686 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003073211-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 6; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 416  
ID ADA85982 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003082693-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 6; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 417  
ID ADA97194 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003082705-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 6; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 418  
ID ADA79498 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003082763-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 6; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 419  
ID ADA87637 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003087345-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 6; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 420  
ID ADB16839 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003087349-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 6; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 421  
ID ADA91931 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003082694-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 6; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 422  
ID ADB14994 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003087351-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 6; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 423  
ID ADB18955 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003073211-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 6; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 424  
ID ADA94170 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.



PN US2003077722-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 6; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 425  
ID ADB20066 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003082691-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 6; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 426  
ID ADB13378 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003082710-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 6; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 427  
ID ABO43401 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003044945-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 6; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 428  
ID ADA74632 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003068798-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 6; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 429  
ID ADB24865 standard; protein; 250 AA.  
DE Human PRO polypeptide SEQ ID NO 506.  
PN US2003077713-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 6; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 430  
ID ADA82389 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003082701-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 6; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 431  
ID ADA75352 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003073216-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 6; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 432  
ID ADA85430 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003082695-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 6; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 433  
ID ADA84878 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003082708-A1.

PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 6; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 434  
ID ADB30134 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003073214-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 6; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 435  
ID ADA80662 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003082761-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 6; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 436  
ID ADA75904 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003082703-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 6; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 437  
ID ADA47129 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003073210-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 6; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 438  
ID ADB25425 standard; protein; 250 AA.  
DE Human PRO polypeptide SEQ ID NO 506.  
PN US2003077715-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 6; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 439  
ID ADA93601 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003077721-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 6; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 440  
ID ADB26951 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003092147-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 6; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 441  
ID ADB31238 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003096386-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 6; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 442  
ID ABJ72448 standard; protein; 250 AA.  
DE Human PRO1279 protein.  
PN US2003027988-A1.  
PD 06-FEB-2003.

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PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 6; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 443
ID ADA61166 standard; protein; 250 AA.
DE Homo sapiens.
PN US2003049817-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 6; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 444
ID ADB24313 standard; protein; 250 AA.
DE Human PRO polypeptide SEQ ID NO 506.
PN US2003077714-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 6; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 445
ID ADA96642 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003082690-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 6; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 446
ID ADA81214 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003082702-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 6; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 447
ID ADA96090 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003082759-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 6; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 448
ID ADB26399 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003082760-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 6; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 449
ID ADB21884 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003082765-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 6; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 450
ID ABO34343 standard; protein; 250 AA.
DE Human secreted/transmembrane polypeptide PRO 1279.
PN US2003044934-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 6; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 451
ID ADA77663 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003068797-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 452
ID ADB18403 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003077710-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 453
ID ADA87086 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003082709-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 454
ID ABO44485 standard; protein; 250 AA.
DE Human secreted/transmembrane protein PRO1279.
PN US2003044841-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 455
ID ADA88189 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003082700-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 456
ID ADA46577 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003054516-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 457
ID ADB28607 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003082699-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 458
ID ADB29159 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003082706-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 459
ID ABO26216 standard; protein; 250 AA.
DE Human protein from novel secreted protein gene 179.
PN US6525174-B1.
PD 25-FEB-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 460
ID ADA77111 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003059909-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
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Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 461  
ID ABO33509 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003073129-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 462  
ID ADA88741 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003073213-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 463  
ID ADA97746 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003082686-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 464  
ID ADB27503 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003022239-A1.  
PD 30-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 465  
ID ADB22436 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003087344-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 466  
ID ABO72150 standard; protein; 250 AA.  
DE Human membrane bound receptor/protein PRO1279 amino acid sequence.  
PN US2003065147-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 467  
ID ADA67127 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003068793-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 468  
ID ADB22988 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003077711-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 469  
ID ADB23761 standard; protein; 250 AA.  
DE Human PRO polypeptide SEQ ID NO 506.  
PN US2003077712-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 470  
ID ADA92483 standard; protein; 250 AA.

DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003082712-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 471  
ID ADB15546 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003087352-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 472  
ID ADB83676 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003073814-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 473  
ID ADB80782 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003088068-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 474  
ID ADB73323 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003096968-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 475  
ID ADB38798 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003082766-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 476  
ID ADB78405 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003092889-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 477  
ID ADB38246 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003087347-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 478  
ID ADB66718 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003082689-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 479  
ID ADB85053 standard; protein; 250 AA.  
DE Human PRO polypeptide #93.

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PN US2003073817-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 480
ID ADB89798 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003082698-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 481
ID ADB90530 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003082762-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 482
ID ADB80596 standard; protein; 250 AA.
DE Ovarian cancer-associated protein #81.
PN WO2002102235-A2.
PD 27-DEC-2002.
PA (BOSB-) EOS BIOTECHNOLOGY INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 483
ID ADB39631 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003082764-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 484
ID ADB78159 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003092886-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 485
ID ADB87225 standard; protein; 250 AA.
DE Human PRO polypeptide #93.
PN US2003088067-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 486
ID ADB84807 standard; protein; 250 AA.
DE Human PRO polypeptide #93.
PN US2003092890-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 487
ID ADB47254 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003082687-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 488
ID ADB83922 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003069397-A1.

PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 489
ID ADB86861 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003082697-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 490
ID ADB73077 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003092887-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 491
ID ADB77466 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003082696-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 492
ID ADB75388 standard; protein; 250 AA.
DE Prostate cancer marker protein.
PN WO2003009814-A2.
PD 06-FEB-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 493
ID ADB34623 standard; protein; 250 AA.
DE Human PRO polypeptide SEQ ID NO 506.
PN US2003077717-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 494
ID ADB35727 standard; protein; 250 AA.
DE Human PRO polypeptide SEQ ID NO 506.
PN US2003077719-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 495
ID ADB34071 standard; protein; 250 AA.
DE Human PRO polypeptide SEQ ID NO 506.
PN US2003077716-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 496
ID ADB35175 standard; protein; 250 AA.
DE Human PRO polypeptide SEQ ID NO 506.
PN US2003077718-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 497
ID ADB36279 standard; protein; 250 AA.
DE Human PRO polypeptide SEQ ID NO 506.
PN US2003077720-A1.
PD 24-APR-2003.
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PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 498  
ID ADC46674 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
FN US2003082692-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 499  
ID ADC18039 standard; protein; 250 AA.  
DE Human PRO polypeptide #51.  
FN US2003064925-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 500  
ID ADC36915 standard; protein; 250 AA.  
DE Human PRO polypeptide #93.  
FN US2003088065-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 501  
ID ADC21905 standard; protein; 250 AA.  
DE Human PRO polypeptide #93.  
FN US2003096969-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 502  
ID ADC50847 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
FN US2003092106-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 503  
ID ADC72094 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
FN US2003092107-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 504  
ID ADC60073 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
FN US2003092105-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 505  
ID ADC49936 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
FN US2003088064-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 506  
ID ADC49135 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
FN US2003088070-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.

Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 507  
ID ADC49652 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
FN US2003088071-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 508  
ID ADC47513 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
FN US2003088072-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 509  
ID ADC53080 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein Seq ID506.  
FN US2003087365-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 510  
ID ADC57434 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein Seq ID506.  
FN US2003087366-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 511  
ID ADC60625 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
FN US2003087367-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 512  
ID ADC51100 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
FN US2003087361-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 513  
ID ADC65627 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
FN US2003087362-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 514  
ID ADC54725 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein Seq ID506.  
FN US2003087363-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 515  
ID ADC53686 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein Seq ID506.  
FN US2003087364-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;

Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 516  
ID ADC59209 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein Seq ID506.  
PN US2003087359-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 517  
ID ADC56087 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein Seq ID506.  
PN US2003087360-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 518  
ID ADC58657 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein Seq ID506.  
PN US2003087346-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 519  
ID ADC47258 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003105288-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 520  
ID ADD03331 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003092104-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 521  
ID ADC90323 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003087348-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 522  
ID ADC69742 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003194770-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 523  
ID ADC48631 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003194773-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 524  
ID ADD10160 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003194776-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 525  
ID ADC78133 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003096972-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 526  
ID ADD04735 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003087354-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 527  
ID ADD06368 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003073816-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 528  
ID ADC80691 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003092103-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 529  
ID ADD11198 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003194774-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 530  
ID ADD10497 standard; protein; 250 AA.  
DE Human secreted/transmembrane PRO polypeptide #104.  
PN US2003105011-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 531  
ID ADC48079 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003194771-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 532  
ID ADC77887 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003088066-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 533  
ID ADC80139 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003087358-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 534  
ID ADC80139 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003087358-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;

ID ADD11457 standard; protein; 250 AA.  
DE Human secreted/transmembrane PRO polypeptide #104.  
PN US2003105013-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 535  
ID ADD09608 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003194775-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 536  
ID ADD50850 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003105291-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 537  
ID ADD41321 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003203438-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 538  
ID ADD52460 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003194769-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 539  
ID ADD51096 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003105290-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 540  
ID ADD70685 standard; protein; 250 AA.  
DE Human secreted/transmembrane protein PRO1279.  
PN US2003099625-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 541  
ID ADD39762 standard; protein; 250 AA.  
DE Human secreted/transmembrane protein PRO1279.  
PN US2003083462-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 542  
ID ADD53200 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003194792-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 543  
ID ADD53752 standard; protein; 250 AA.

DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003203437-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 544  
ID ADD70208 standard; protein; 250 AA.  
DE Human secreted/transmembrane protein PRO1279.  
PN US2003054406-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 545  
ID ADD37250 standard; protein; 250 AA.  
DE Human secreted/transmembrane PRO polypeptide #104.  
PN US2003105012-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 546  
ID ADD38329 standard; protein; 250 AA.  
DE Human secreted/transmembrane protein PRO1279.  
PN US2003096955-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 547  
ID ADD39285 standard; protein; 250 AA.  
DE Human secreted/transmembrane protein PRO1279.  
PN US2003096954-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 548  
ID ADD51908 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003194779-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 549  
ID ADD02707 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003203431-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 550  
ID ADD50577 standard; protein; 250 AA.  
DE Human PRO polypeptide #93.  
PN US2003096971-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 551  
ID ADD02141 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003203430-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 552  
ID ADD54323 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.

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PN US2003203432-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 553
ID ADD50331 standard; protein; 250 AA.
DE Human PRO polypeptide #93.
PN US2003096970-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 554
ID ADD38808 standard; protein; 250 AA.
DE Human secreted/transmembrane protein PRO1279.
PN US2003092061-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 555
ID ADD40239 standard; protein; 250 AA.
DE Human secreted/transmembrane protein PRO1279.
PN US2003082627-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 556
ID ADD51342 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003105289-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 557
ID ADE50460 standard; protein; 250 AA.
DE Human secreted/transmembrane protein PRO1279.
PN US2003069179-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 558
ID ADD92640 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003199030-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 559
ID ADD91536 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003199055-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 560
ID ADE04150 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003199057-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 561
ID ADE20072 standard; protein; 250 AA.
DE Human secreted/transmembrane protein PRO1279.
PN US2003092883-A1.

PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 562
ID ADE32447 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003194765-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 563
ID ADE22379 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003199056-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 564
ID ADD79603 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003203428-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 565
ID ADE42139 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003194772-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 566
ID ADE17956 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003199023-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 567
ID ADD92088 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003199053-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 568
ID ADE33551 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003194767-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 569
ID ADE34103 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003194791-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 7; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 570
ID ADD80155 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003207417-A1.
PD 06-NOV-2003.
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PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 571  
ID ADE49983 standard; protein; 250 AA.  
DE Human secreted/transmembrane protein PRO1279.  
PN US2003082626-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 572  
ID ADD93192 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003194768-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 573  
ID ADE19612 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003199025-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 574  
ID ADE21541 standard; protein; 250 AA.  
DE Human secreted/transmembrane protein PRO1279.  
PN US2003082628-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 575  
ID ADE19060 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003199026-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 576  
ID ADE43256 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003199033-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 577  
ID ADD96045 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003199059-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 578  
ID ADE22931 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003199064-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 579  
ID ADD79049 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003203429-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.

Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 580  
ID ADE32999 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003194766-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 581  
ID ADE42691 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003199032-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 582  
ID ADD80707 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003207418-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 583  
ID ADD89735 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003199028-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 584  
ID ADE41019 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003199031-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 585  
ID ADE04818 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003199034-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 586  
ID ADE92947 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003194777-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 587  
ID ADF29966 standard; protein; 250 AA.  
DE Human secreted/transmembrane protein PRO1279.  
PN US2003204053-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 588  
ID ADF58059 standard; protein; 250 AA.  
DE Human secreted/transmembrane protein PRO1279.  
PN US2003204054-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 589  
ID ADD79049 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003203429-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.

Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 589  
ID ADG21656 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003207386-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 590  
ID ADG32297 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003207384-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 591  
ID ADF97632 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003207370-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 592  
ID ADG80696 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003207373-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 593  
ID ADG80144 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003207372-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 594  
ID ADH5436 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003207381-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 595  
ID ADH5988 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003207379-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 596  
ID ADH9363 standard; protein; 250 AA.  
DE Human secreted/transmembrane protein PRO1279.  
PN US2003065142-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 597  
ID ADI64207 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003207385-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 598  
ID ADI65156 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003207386-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 599  
ID ADH82069 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003207388-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 600  
ID ADH81517 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003207377-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 601  
ID ADM82686 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003087355-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 602  
ID ADN16085 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003087353-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 603  
ID ADN16714 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003087385-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 604  
ID ADN39242 standard; protein; 250 AA.  
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:560.  
PN WC2003042661-A2.  
PD 22-MAY-2003.  
PA (EOSB-) EOS BIOTECHNOLOGY INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 605  
ID ADN15533 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003087356-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 606  
ID ADN14981 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003087357-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 607

ID ADI6355 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US200320738-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 608  
ID ADC4889 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003092888-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 609  
ID ADC81243 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003092115-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 610  
ID ADE21060 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003100735-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 611  
ID ADE05904 standard; protein; 250 AA.  
DE Human PRO polypeptide #93.  
PN US2003100728-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 612  
ID ADD76691 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003100087-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 613  
ID ADD75133 standard; protein; 250 AA.  
DE Human PRO polypeptide #93.  
PN US2003100712-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 614  
ID ADD75879 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003100717-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 615  
ID ADD85111 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003100722-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 616  
ID ADD86937 standard; protein; 250 AA.

DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003100738-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 617  
ID ADE20814 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003100734-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 618  
ID ADE39111 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003096362-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 619  
ID ADD88055 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003092113-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 620  
ID ADD86459 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003203440-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 621  
ID ADE05658 standard; protein; 250 AA.  
DE Human PRO polypeptide #93.  
PN US2003100727-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 622  
ID ADD73643 standard; protein; 250 AA.  
DE Human PRO polypeptide #93.  
PN US2003100711-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 623  
ID ADE75907 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003211571-A1.  
PD 13-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 624  
ID ADD78483 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003100737-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 625  
ID ADE41458 standard; protein; 250 AA.  
DE Human secreted/transmembrane PRO polypeptide #104.

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PN US2003100497-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 626
ID ADE23483 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003092108-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 627
ID ADE21306 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003100736-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 628
ID ADD77421 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003100732-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 629
ID ADE20568 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003100733-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 630
ID ADD75633 standard; protein; 250 AA.
DE Human PRO polypeptide #93.
PN US2003100064-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 631
ID ADD74149 standard; protein; 250 AA.
DE Human PRO polypeptide #93.
PN US2003100708-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 632
ID ADD74395 standard; protein; 250 AA.
DE Human PRO polypeptide #93.
PN US2003100709-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 633
ID ADD76125 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003100718-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 634
ID ADD85617 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003100721-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 635
ID ADE24035 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003092110-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 636
ID ADE24678 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003092111-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 637
ID ADD87503 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003203439-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 638
ID ADE05166 standard; protein; 250 AA.
DE Human PRO polypeptide #93.
PN US2003100726-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 639
ID ADD75379 standard; protein; 250 AA.
DE Human PRO polypeptide #93.
PN US2003100714-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 640
ID ADD76923 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003100715-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 641
ID ADD86691 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003100719-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 642
ID ADE89369 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003199062-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 643
ID ADD78159 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003100731-A1.
PD 29-MAY-2003.
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PA (GETH ) GENENTECH INC.  
 Query Match 45.0%; Score 618.5; DB 8; Length 250;  
 Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
 RESULT 644  
 ID ADE18508 standard; protein; 250 AA.  
 DE Human PRO polypeptide #253.  
 PN US2003194794-A1.  
 PD 16-OCT-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 45.0%; Score 618.5; DB 8; Length 250;  
 Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
 RESULT 645  
 ID ADE88817 standard; protein; 250 AA.  
 DE Human PRO polypeptide #253.  
 PN US2003199054-A1.  
 PD 23-OCT-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 45.0%; Score 618.5; DB 8; Length 250;  
 Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
 RESULT 646  
 ID ADD7667 standard; protein; 250 AA.  
 DE Novel human secreted and transmembrane protein PRO1279.  
 PN US2003100729-A1.  
 PD 29-MAY-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 45.0%; Score 618.5; DB 8; Length 250;  
 Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
 RESULT 647  
 ID ADD7913 standard; protein; 250 AA.  
 DE Novel human secreted and transmembrane protein PRO1279.  
 PN US2003100730-A1.  
 PD 29-MAY-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 45.0%; Score 618.5; DB 8; Length 250;  
 Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
 RESULT 648  
 ID ADD85371 standard; protein; 250 AA.  
 DE Novel human secreted and transmembrane protein PRO1279.  
 PN US2003100725-A1.  
 PD 29-MAY-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 45.0%; Score 618.5; DB 8; Length 250;  
 Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
 RESULT 649  
 ID ADD73903 standard; protein; 250 AA.  
 DE Human PRO polypeptide #93.  
 PN US2003100710-A1.  
 PD 29-MAY-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 45.0%; Score 618.5; DB 8; Length 250;  
 Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
 RESULT 650  
 ID ADD74641 standard; protein; 250 AA.  
 DE Human PRO polypeptide #93.  
 PN US2003100713-A1.  
 PD 29-MAY-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 45.0%; Score 618.5; DB 8; Length 250;  
 Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
 RESULT 651  
 ID ADD77169 standard; protein; 250 AA.  
 DE Novel human secreted and transmembrane protein PRO1279.  
 PN US2003100716-A1.  
 PD 29-MAY-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 45.0%; Score 618.5; DB 8; Length 250;  
 Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
 RESULT 652  
 ID ADD85863 standard; protein; 250 AA.  
 DE Novel human secreted and transmembrane protein PRO1279.  
 PN US2003100720-A1.  
 PD 29-MAY-2003.  
 PA (GETH ) GENENTECH INC.

Query Match 45.0%; Score 618.5; DB 8; Length 250;  
 Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
 RESULT 653  
 ID ADE05412 standard; protein; 250 AA.  
 DE Human PRO polypeptide #93.  
 PN US2003100723-A1.  
 PD 29-MAY-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 45.0%; Score 618.5; DB 8; Length 250;  
 Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
 RESULT 654  
 ID ADD74887 standard; protein; 250 AA.  
 DE Human PRO polypeptide #93.  
 PN US2003100724-A1.  
 PD 29-MAY-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 45.0%; Score 618.5; DB 8; Length 250;  
 Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
 RESULT 655  
 ID ADE96543 standard; protein; 250 AA.  
 DE Human secreted/transmembrane protein PRO1279.  
 PN US2003195347-A1.  
 PD 16-OCT-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 45.0%; Score 618.5; DB 8; Length 250;  
 Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
 RESULT 656  
 ID ADE94837 standard; protein; 250 AA.  
 DE Human PRO polypeptide #253.  
 PN US2003199027-A1.  
 PD 23-OCT-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 45.0%; Score 618.5; DB 8; Length 250;  
 Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
 RESULT 657  
 ID ADE91248 standard; protein; 250 AA.  
 DE Human PRO polypeptide #253.  
 PN US2003199061-A1.  
 PD 23-OCT-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 45.0%; Score 618.5; DB 8; Length 250;  
 Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
 RESULT 658  
 ID ADF25854 standard; protein; 250 AA.  
 DE Human secreted/transmembrane protein PRO1279.  
 PN US2003199675-A1.  
 PD 23-OCT-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 45.0%; Score 618.5; DB 8; Length 250;  
 Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
 RESULT 659  
 ID ADE95389 standard; protein; 250 AA.  
 DE Human PRO polypeptide #253.  
 PN US2003199052-A1.  
 PD 23-OCT-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 45.0%; Score 618.5; DB 8; Length 250;  
 Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
 RESULT 660  
 ID ADE93499 standard; protein; 250 AA.  
 DE Human PRO polypeptide #253.  
 PN US2003199060-A1.  
 PD 23-OCT-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 45.0%; Score 618.5; DB 8; Length 250;  
 Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
 RESULT 661  
 ID ADF24753 standard; protein; 250 AA.  
 DE Human secreted/transmembrane protein PRO1279.  
 PN US2003198993-A1.  
 PD 23-OCT-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 45.0%; Score 618.5; DB 8; Length 250;

Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 662  
ID ADF29489 standard; protein; 250 AA.  
DE Human secreted/transmembrane protein PRO1279.  
PN US2003203401-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 663  
ID ADF35080 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003199029-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 664  
ID ADE97020 standard; protein; 250 AA.  
DE Human secreted/transmembrane protein PRO1279.  
PN US2003195334-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 665  
ID ADE92395 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003199051-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 666  
ID ADE90696 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003199063-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 667  
ID ADE91843 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003199058-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 668  
ID ADG05699 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003096959-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 669  
ID ADG27253 standard; protein; 250 AA.  
DE Human PRO polypeptide #93.  
PN US2003096962-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 670  
ID ADG02422 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003207352-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;

RESULT 671  
ID ADG22208 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003207360-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 672  
ID ADG20278 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003207376-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 673  
ID ADF98184 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003207422-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 674  
ID ADG24401 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003207426-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 675  
ID ADF98755 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003208055-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 676  
ID ADG03586 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003207351-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 677  
ID ADF99307 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003207353-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 678  
ID ADG16892 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003207359-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 679  
ID ADG05351 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003207375-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 680  
ID ADG02422 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003207352-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;

ID ADG19618 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003207425-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 681  
ID ADG11316 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003096967-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 682  
ID ADG13455 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003207357-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 683  
ID ADG08512 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003207424-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 684  
ID ADG15682 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003219885-A1.  
PD 27-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 685  
ID ADG12095 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003096963-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 686  
ID ADF97080 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003207371-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 687  
ID ADG06265 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003207374-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 688  
ID ADG23049 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003207389-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 689  
ID ADG04138 standard; protein; 250 AA.

DE Human PRO polypeptide #253.  
PN US2003207423-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 690  
ID ADG25039 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003207427-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 691  
ID ADF94652 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003096964-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 692  
ID ADG07336 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003207350-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 693  
ID ADG07888 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003207356-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 694  
ID ADG06748 standard; protein; 250 AA.  
DE Human PRO polypeptide #93.  
PN US2003096966-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 695  
ID ADG55383 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003194778-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 696  
ID ADG61047 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003207390-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 697  
ID ADG62151 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003207428-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 698  
ID ADH03058 standard; protein; 250 AA.  
DE Human secreted/transmembrane protein PRO1279.

PN US2003216562-A1.  
PD 20-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 699  
ID ADG82352 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003207358-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 700  
ID ADG57591 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003207362-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 701  
ID ADG57039 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003207364-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 702  
ID ADG55935 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003207365-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 703  
ID ADG58695 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003207368-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 704  
ID ADG71061 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003207420-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 705  
ID ADH04012 standard; protein; 250 AA.  
DE Human secreted/transmembrane protein PRO1279.  
PN US2003220471-A1.  
PD 27-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 706  
ID ADH03535 standard; protein; 250 AA.  
DE Human secreted/transmembrane protein PRO1279.  
PN US2003224478-A1.  
PD 04-DEC-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 707  
ID ADH39092 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003096965-A1.

PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 708  
ID ADG58143 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003207363-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 709  
ID ADG53727 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003207415-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 710  
ID ADG71613 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003207421-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 711  
ID ADG81800 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003207805-A1.  
PD 06-NOV-2003.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 712  
ID ADH30762 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003077723-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 713  
ID ADH12129 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003207419-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 714  
ID ADG52551 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003207414-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 715  
ID ADG54279 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003207416-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 716  
ID ADG81248 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003194793-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.



Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 717  
ID ADG56487 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003207366-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 718  
ID ADH12753 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003207378-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 719  
ID ADG61599 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003207429-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 720  
ID ADH28686 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003022331-A1.  
PD 30-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 721  
ID ADG54831 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003207367-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 722  
ID ADG59871 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003207369-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 723  
ID ADH43641 standard; protein; 250 AA.  
DE Human PRO polypeptide #104.  
PN US2003224984-A1.  
PD 04-DEC-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 724  
ID ADG34182 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2004006206-A1.  
PD 08-JAN-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 725  
ID ADH04489 standard; protein; 250 AA.  
DE Human secreted/transmembrane protein PRO1279.  
PN US2004005626-A1.  
PD 08-JAN-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;

Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 726  
ID ADI81295 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003207361-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 727  
ID ADI33652 standard; protein; 250 AA.  
DE Human PRO polypeptide #93.  
PN US2003096960-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 728  
ID ADH69746 standard; protein; 250 AA.  
DE Human PRO polypeptide #93.  
PN US2004019183-A1.  
PD 29-JAN-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 729  
ID ADH61490 standard; protein; 250 AA.  
DE Human secreted/transmembrane protein PRO1279.  
PN US2004014130-A1.  
PD 22-JAN-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 730  
ID ADG10038 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2004009548-A1.  
PD 15-JAN-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 731  
ID ADI15509 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003207382-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 732  
ID ADG09386 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2004009547-A1.  
PD 15-JAN-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 733  
ID ADI14841 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003207383-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 734  
ID ADI29907 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003096961-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;

RESULT 735  
ID ADL94689 standard; protein; 250 AA.  
DE Human secreted/transmembrane protein PRO1279.  
PN US2004073015-A1.  
PD 15-APR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 736  
ID ADM27304 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2004044179-A1.  
PD 04-MAR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 737  
ID ADJ63717 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2004039164-A1.  
PD 26-FEB-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 738  
ID ADJ77612 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2004038336-A1.  
PD 26-FEB-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 739  
ID ADK82986 standard; protein; 250 AA.  
DE Human PRO polypeptide #104.  
PN US2004043927-A1.  
PD 04-MAR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 740  
ID ADK66662 standard; protein; 250 AA.  
DE Human PRO polypeptide #93.  
PN US2004044180-A1.  
PD 04-MAR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 741  
ID ADJ65734 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2004038335-A1.  
PD 26-FEB-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 742  
ID ADM27870 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2004048333-A1.  
PD 11-MAR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 743  
ID ADM42594 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2004058424-A1.  
PD 25-MAR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 744  
ID AAY43636 standard; protein; 282 AA.

ID ADL94689 standard; protein; 250 AA.  
DE Human secreted/transmembrane protein PRO1279.  
PN US2004073015-A1.  
PD 15-APR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 745  
ID ADM28456 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2004077064-A1.  
PD 22-APR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 746  
ID ADI95938 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003077659-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 747  
ID ADI96490 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US20030207354-A1.  
PD 08-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 748  
ID ADR72632 standard; protein; 250 AA.  
DE Human renal cell carcinoma-related kallikrein 11 (hK11) protein 2.  
PN WO2004077060-A2.  
PD 10-SEP-2004.  
PA (MOUN ) MOUNT SINAI HOSPITAL.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 749  
ID ADR72890 standard; protein; 250 AA.  
DE Human ovarian cancer-related tumour marker kallikrein 11 (hK11) protein 2.  
PN WO2004075713-A2.  
PD 10-SEP-2004.  
PA (MOUN ) MOUNT SINAI HOSPITAL.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 750  
ID ADS34892 standard; protein; 250 AA.  
DE Human autoimmune disease-related protein - SEQ ID 106.  
PN WO2004083403-A2.  
PD 30-SEP-2004.  
PA (APPL-) APPLERA CORP.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 751  
ID AAY42439 standard; protein; 282 AA.  
DE CASB12 amino acid sequence.  
PN WO9943055-A1.  
PD 30-SEP-1999.  
PA (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.  
Query Match 45.0%; Score 618.5; DB 2; Length 282;  
Best Local Similarity 48.2%; Pred. No. 9.9e-40;  
RESULT 752  
ID AAB11712 standard; protein; 282 AA.  
DE Human serine protease BSSP6 (hBSSP6) SEQ ID NO:2.  
PN WO2000031257-A1.  
PD 02-JUN-2000.  
PA (FUSO ) FUSO PHARM IND LTD.  
Query Match 45.0%; Score 618.5; DB 3; Length 282;  
Best Local Similarity 48.2%; Pred. No. 9.9e-40;  
RESULT 753  
ID AAY43636 standard; protein; 282 AA.

DE A human prostate-associated serum protease (PRASP).  
PN WO9941387-A2.  
PD 19-AUG-1999.  
PA (INCY-) INCYTE PHARM INC.  
Query Match 45.0%; Score 618.5; DB 3; Length 282;  
Best Local Similarity 48.2%; Pred. No. 9.9e-40;  
RESULT 754  
ID ADN11325 standard; protein; 282 AA.  
DE Human kallikrein-11, marker for prostate cancer.  
PN WO2004029616-A2.  
PD 08-APR-2004.  
PA (MOUN) MOUNT SINAI HOSPITAL.  
Query Match 45.0%; Score 618.5; DB 8; Length 282;  
Best Local Similarity 48.2%; Pred. No. 9.9e-40;  
RESULT 755  
ID ADQ17587 standard; protein; 282 AA.  
DE Human soft tissue sarcoma-upregulated protein - SEQ ID 404.  
PN WO2004048938-A2.  
PD 10-JUN-2004.  
PA (MOUN) MOUNT SINAI HOSPITAL.  
Query Match 45.0%; Score 618.5; DB 8; Length 282;  
Best Local Similarity 48.2%; Pred. No. 9.9e-40;  
RESULT 756  
ID ADR72631 standard; protein; 282 AA.  
DE Human renal cell carcinoma-related kallikrein 11 (hk11) protein 1.  
PN WO2004077060-A2.  
PD 10-SEP-2004.  
PA (MOUN) MOUNT SINAI HOSPITAL.  
Query Match 45.0%; Score 618.5; DB 8; Length 282;  
Best Local Similarity 48.2%; Pred. No. 9.9e-40;  
RESULT 757  
ID ADR72889 standard; protein; 282 AA.  
DE Human ovarian cancer-related tumour marker kallikrein 11 (hk11) protein1.  
PN WO2004075713-A2.  
PD 10-SEP-2004.  
PA (MOUN) MOUNT SINAI HOSPITAL.  
Query Match 45.0%; Score 618.5; DB 8; Length 282;  
Best Local Similarity 48.2%; Pred. No. 9.9e-40;  
RESULT 758  
ID ADS34893 standard; protein; 282 AA.  
DE Human autoimmune disease-related protein - SEQ ID 107.  
PN WO2004083403-A2.  
PD 30-SEP-2004.  
PA (APPL-) APPLERA CORP.  
Query Match 45.0%; Score 618.5; DB 8; Length 282;  
Best Local Similarity 48.2%; Pred. No. 9.9e-40;  
RESULT 759  
ID AAY42440 standard; protein; 281 AA.  
DE CASB12 polypeptide derived from Expressed Sequence Tag products.  
PN WO9949055-A1.  
PD 30-SEP-1999.  
PA (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.  
Query Match 44.6%; Score 612.5; DB 2; Length 281;  
Best Local Similarity 48.0%; Pred. No. 2.8e-39;  
RESULT 760  
ID AAB36482 standard; protein; 288 AA.  
DE Fusion gene with human serine protease catalytic domain protein #13.  
PN WO200066709-A2.  
PD 09-NOV-2000.  
PA (ORTH) ORTHO-MCNEIL PHARM RES INC.  
Query Match 43.9%; Score 602.5; DB 3; Length 288;  
Best Local Similarity 51.1%; Pred. No. 1.7e-38;  
RESULT 761  
ID AAB67542 standard; protein; 288 AA.  
DE Amino acid sequence of catalytic domain in PFEK1-6XHIS-TAG.  
PN WO200116289-A2.  
PD 08-MAR-2001.  
PA (ORTH) ORTHO-MCNEIL PHARM INC.  
Query Match 43.9%; Score 602.5; DB 4; Length 288;  
Best Local Similarity 51.1%; Pred. No. 1.7e-38;  
RESULT 762  
ID AAY36093 standard; protein; 250 AA.  
DE Extended human secreted protein sequence, SEQ ID NO. 478.

PN WO9931236-A2.  
PD 24-JUN-1999.  
PA (GEST-) GENSET.  
Query Match 43.8%; Score 601.5; DB 2; Length 250;  
Best Local Similarity 47.4%; Pred. No. 1.8e-38;  
RESULT 763  
ID ADP19401 standard; protein; 250 AA.  
DE Human secreted polypeptide #252.  
PN US2004110939-A1.  
PD 10-JUN-2004.  
PA (GEST) GENSET SA.  
Query Match 43.8%; Score 601.5; DB 8; Length 250;  
Best Local Similarity 47.4%; Pred. No. 1.8e-38;  
RESULT 764  
ID AAB11714 standard; protein; 275 AA.  
DE Human serine protease BSSP6 (hBSSP6) SEQ ID NO:6.  
PN WO200031257-A1.  
PD 02-JUN-2000.  
PA (FUSO) FUSO PHARM IND LTD.  
Query Match 43.7%; Score 601; DB 3; Length 275;  
Best Local Similarity 44.2%; Pred. No. 2.1e-38;  
RESULT 765  
ID AAU82732 standard; protein; 320 AA.  
DE Amino acid sequence of novel human protease #31.  
PN WO200200860-A2.  
PD 03-JAN-2002.  
PA (SUGE-) SUGEN INC.  
Query Match 43.6%; Score 599.5; DB 5; Length 320;  
Best Local Similarity 46.4%; Pred. No. 3.3e-38;  
RESULT 766  
ID AAE19166 standard; protein; 320 AA.  
DE Human protease, PRTS-3 protein.  
PN WO200208396-A2.  
PD 31-JAN-2002.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match 43.6%; Score 599.5; DB 5; Length 320;  
Best Local Similarity 46.4%; Pred. No. 3.3e-38;  
RESULT 767  
ID ADI17075 standard; protein; 225 AA.  
DE Murine NOVX protein homologue SeqID 611.  
PN WO200268649-A2.  
PD 06-SEP-2002.  
PA (CURA-) CURAGEN CORP.  
Query Match 43.6%; Score 599; DB 5; Length 225;  
Best Local Similarity 49.8%; Pred. No. 2.5e-38;  
RESULT 768  
ID AAU79390 standard; protein; 256 AA.  
DE Novel human kallikrein KLK15.  
PN WO200214485-A2.  
PD 21-FEB-2002.  
PA (MOUN) MOUNT SINAI HOSPITAL.  
Query Match 43.6%; Score 599; DB 5; Length 256;  
Best Local Similarity 47.1%; Pred. No. 2.8e-38;  
RESULT 769  
ID ADN10932 standard; protein; 256 AA.  
DE Human kallikrein 15, marker of endocrine cancer.  
PN WO2004029285-A2.  
PD 08-APR-2004.  
PA (MOUN) MOUNT SINAI HOSPITAL.  
Query Match 43.6%; Score 599; DB 8; Length 256;  
Best Local Similarity 47.1%; Pred. No. 2.8e-38;  
RESULT 770  
ID AAB36483 standard; protein; 289 AA.  
DE Fusion gene with human serine protease catalytic domain protein #14.  
PN WO200066709-A2.  
PD 09-NOV-2000.  
PA (ORTH) ORTHO-MCNEIL PHARM RES INC.  
Query Match 43.6%; Score 598.5; DB 3; Length 289;  
Best Local Similarity 49.1%; Pred. No. 3.5e-38;  
RESULT 771  
ID AAB67543 standard; protein; 289 AA.  
DE Amino acid sequence of catalytic domain in PFEK1-6XHIS-TAG.  
PN WO200116289-A2.

PD 08-MAR-2001.  
PA (ORTH ) ORTHO-MCNEIL PHARM INC.  
Query Match 43.6%; Score 598.5; DB 4; Length 289;  
Best Local Similarity 49.1%; Pred. No. 3.5e-36;  
RESULT 772  
ID AAE08017 standard; protein; 248 AA.  
DE Human PSI33 consensus protein sequence.  
PN US6232456-B1.  
PD 15-MAY-2001.  
PA (ABBOTT ) ABBOTT LAB.  
Query Match 43.5%; Score 597.5; DB 4; Length 248;  
Best Local Similarity 47.8%; Pred. No. 3.6e-36;  
RESULT 773  
ID AAB11713 standard; protein; 276 AA.  
DE Mouse serine protease BSSP6 (MBSSP6) SEQ ID NO:4.  
PN WO200031257-A1.  
PD 02-JUN-2000.  
PA (FUSO ) FUSO PHARM IND LTD.  
Query Match 43.5%; Score 597.5; DB 3; Length 276;  
Best Local Similarity 47.0%; Pred. No. 4e-38;  
RESULT 774  
ID ADC31389 standard; protein; 298 AA.  
DE Human novel polypeptide sequence, SEQ ID NO:1471.  
PN WO2003029271-A2.  
PD 10-APR-2003.  
PA (HYSEQ-) HYSEQ INC.  
Query Match 43.3%; Score 595; DB 7; Length 298;  
Best Local Similarity 48.1%; Pred. No. 6.8e-36;  
RESULT 775  
ID ADI17077 standard; protein; 260 AA.  
DE Human NOVX protein homologue SegID 613.  
PN WO200268649-A2.  
PD 06-SEP-2002.  
PA (CURAGEN ) CURAGEN CORP.  
Query Match 43.2%; Score 593.5; DB 5; Length 260;  
Best Local Similarity 48.6%; Pred. No. 7.7e-36;  
RESULT 776  
ID AAB21312 standard; protein; 228 AA.  
DE Human TLSP.  
PN WO200053776-A2.  
PD 14-SEP-2000.  
PA (MOUNT ) MOUNT SINAI HOSPITAL.  
Query Match 43.1%; Score 592; DB 3; Length 228;  
Best Local Similarity 49.3%; Pred. No. 8.7e-38;  
RESULT 777  
ID AA08475 standard; protein; 247 AA.  
DE Porcine trypsinogen.  
PN WO9700316-A1.  
PD 03-JAN-1997.  
PA (NOVO ) NOVO-NORDISK AS.  
Query Match 41.7%; Score 573; DB 2; Length 247;  
Best Local Similarity 45.6%; Pred. No. 2.8e-36;  
RESULT 778  
ID ABB98258 standard; protein; 247 AA.  
DE Pig trypsinogen SEQ ID NO 1.  
PN WO200261064-A2.  
PD 08-AUG-2002.  
PA (HOFF ) ROCHE DIAGNOSTICS GMBH.  
PA (HOFF ) ROCHE DIAGNOSTICS GMBH. & CO AG F.  
Query Match 41.7%; Score 573; DB 5; Length 247;  
Best Local Similarity 45.6%; Pred. No. 2.8e-36;  
RESULT 779  
ID ADJ92132 standard; protein; 247 AA.  
DE Pig pro-trypsin.  
PN US2004043455-A1.  
PD 04-MAR-2004.  
PA (NOVO ) NOVOZYMES BIOTECH INC.  
Query Match 41.7%; Score 573; DB 8; Length 247;  
Best Local Similarity 45.6%; Pred. No. 2.8e-36;  
RESULT 780  
ID AAB21306 standard; protein; 251 AA.  
DE Human KLK-L6 protein #2.  
PN WO200053776-A2.

PD 14-SEP-2000.  
PA (MOUNT ) MOUNT SINAI HOSPITAL.  
Query Match 41.4%; Score 569.5; DB 3; Length 251;  
Best Local Similarity 46.9%; Pred. No. 5.2e-36;  
RESULT 781  
ID ADN10930 standard; protein; 251 AA.  
DE Human kallikrein 14, marker of endocrine cancer.  
PN WO2004029285-A2.  
PD 08-APR-2004.  
PA (MOUNT ) MOUNT SINAI HOSPITAL.  
Query Match 41.4%; Score 569.5; DB 8; Length 251;  
Best Local Similarity 46.9%; Pred. No. 5.2e-36;  
RESULT 782  
ID ABJ26666 standard; protein; 267 AA.  
DE Human protein modification + maintenance molecule protein SEQ ID NO 20.  
PN WO2003000844-A2.  
PD 03-JAN-2003.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match 41.4%; Score 569.5; DB 6; Length 267;  
Best Local Similarity 46.9%; Pred. No. 5.6e-36;  
RESULT 783  
ID AAB21298 standard; protein; 250 AA.  
DE Human KLK-L3 protein #2.  
PN WO200053776-A2.  
PD 14-SEP-2000.  
PA (MOUNT ) MOUNT SINAI HOSPITAL.  
Query Match 41.4%; Score 568.5; DB 3; Length 250;  
Best Local Similarity 46.7%; Pred. No. 6.2e-36;  
RESULT 784  
ID ABP64969 standard; protein; 250 AA.  
DE Human protein SEQ ID 629.  
PN WO200259260-A2.  
PD 01-AUG-2002.  
PA (HYSEQ-) HYSEQ INC.  
Query Match 41.4%; Score 568.5; DB 5; Length 250;  
Best Local Similarity 46.7%; Pred. No. 6.2e-36;  
RESULT 785  
ID ABR55400 standard; protein; 250 AA.  
DE Amino acid sequence of human kallikrein 9 (HK9).  
PN WO2003033731-A2.  
PD 24-APR-2003.  
PA (MOUNT ) MOUNT SINAI HOSPITAL.  
Query Match 41.4%; Score 568.5; DB 6; Length 250;  
Best Local Similarity 46.7%; Pred. No. 6.2e-36;  
RESULT 786  
ID ADN05516 standard; protein; 250 AA.  
DE Antipeptidic protein sequence #924.  
PN WO2004028479-A2.  
PD 08-APR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 41.4%; Score 568.5; DB 8; Length 250;  
Best Local Similarity 46.7%; Pred. No. 6.2e-36;  
RESULT 787  
ID AAB21300 standard; protein; 277 AA.  
DE Human KLK-L4 protein #2.  
PN WO200053776-A2.  
PD 14-SEP-2000.  
PA (MOUNT ) MOUNT SINAI HOSPITAL.  
Query Match 41.3%; Score 567; DB 3; Length 277;  
Best Local Similarity 46.8%; Pred. No. 9e-36;  
RESULT 788  
ID ABO00554 standard; protein; 277 AA.  
DE Novel human polypeptide #141.  
PN WO2003023013-A2.  
PD 20-MAR-2003.  
PA (HYSEQ-) HYSEQ INC.  
Query Match 41.3%; Score 567; DB 6; Length 277;  
Best Local Similarity 46.8%; Pred. No. 9e-36;  
RESULT 789  
ID ADL71094 standard; protein; 277 AA.  
DE Human kallikrein 13 protein SEQ ID NO:1.  
PN WO2004021009-A2.  
PD 11-MAR-2004.

PA (MOUN ) MOUNT SINAI HOSPITAL.  
Query Match 41.1%; Score 567; DB 8; Length 277;  
Best Local Similarity 46.8%; Pred. No. 9e-36;  
RESULT 790  
ID ADN04184 standard; protein; 277 AA.  
DE Antipsoiratic protein sequence #287.  
FN WO2004028479-A2.  
PD 08-APR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 41.3%; Score 567; DB 8; Length 277;  
Best Local Similarity 46.8%; Pred. No. 9e-36;  
RESULT 791  
ID ADRI4575 standard; protein; 277 AA.  
DE Human NF-kappaB pathway-associated protein SeqID576.  
FN WO2004065577-A2.  
PD 05-AUG-2004.  
PA (BRIM ) BRISTOL-MYERS SQUIBB CO.  
Query Match 41.3%; Score 567; DB 8; Length 277;  
Best Local Similarity 46.8%; Pred. No. 9e-36;  
RESULT 792  
ID AAU16971 standard; protein; 251 AA.  
DE Human novel secreted protein, SEQ ID 212.  
FN WO200155441-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 41.2%; Score 566.5; DB 4; Length 251;  
Best Local Similarity 46.9%; Pred. No. 8.9e-36;  
RESULT 793  
ID AAU23217 standard; protein; 247 AA.  
DE Novel human enzyme polypeptide #303.  
FN WO200155301-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 41.1%; Score 564.5; DB 4; Length 247;  
Best Local Similarity 46.9%; Pred. No. 1.3e-35;  
RESULT 794  
ID AAY16777 standard; protein; 293 AA.  
DE Human keratinocyte derived protease (KDP).  
FN WO9918219-A1.  
PD 15-APR-1999.  
PA (PROC ) PROCTER & GAMBLE CO.  
Query Match 41.1%; Score 564.5; DB 2; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 795  
ID AAY30524 standard; protein; 293 AA.  
DE Human PDSP-1 protein.  
FN WO9946391-A2.  
PD 16-SEP-1999.  
PA (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.  
Query Match 41.1%; Score 564.5; DB 2; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 796  
ID AAY38412 standard; protein; 293 AA.  
DE Human secreted protein encoded by gene No. 27.  
FN WO9935158-A1.  
PD 15-JUL-1999.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 41.1%; Score 564.5; DB 2; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 797  
ID AAY38426 standard; protein; 293 AA.  
DE Human secreted protein encoded by gene No. 27.  
FN WO9935158-A1.  
PD 15-JUL-1999.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 41.1%; Score 564.5; DB 2; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 798  
ID AAY66726 standard; protein; 293 AA.  
DE Membrane-bound protein PRO1132.  
FN WO9963088-A2.  
PD 09-DEC-1999.  
PA (GETH ) GENENTECH INC.

Query Match 41.1%; Score 564.5; DB 3; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 799  
ID AAB21296 standard; protein; 293 AA.  
DE Human KIX-L2 protein.  
FN WO200053776-A2.  
PD 14-SEP-2000.  
PA (MOUN ) MOUNT SINAI HOSPITAL.  
Query Match 41.1%; Score 564.5; DB 3; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 800  
ID AAU12399 standard; protein; 293 AA.  
DE Human PRO1132 polypeptide sequence.  
FN WO200140466-A2.  
PD 07-JUN-2001.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 4; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 801  
ID AAB65249 standard; protein; 293 AA.  
DE Human PRO1132 (UNQ570) protein sequence SEQ ID NO:309.  
FN WO200073454-A1.  
PD 07-DEC-2000.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 4; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 802  
ID AAU81966 standard; protein; 293 AA.  
DE Human PRO1132.  
FN WO200109327-A2.  
PD 08-FEB-2001.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 5; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 803  
ID ABUS8064 standard; protein; 293 AA.  
DE Human PRO polypeptide #96.  
FN US2003027163-A1.  
PD 06-FEB-2003.  
Query Match 41.1%; Score 564.5; DB 6; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 804  
ID ABUS9142 standard; protein; 293 AA.  
DE Novel human secreted or transmembrane protein PRO1132.  
FN US2002132252-A1.  
PD 19-SEP-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 6; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 805  
ID ABUS2654 standard; protein; 293 AA.  
DE Human secreted/transmembrane protein PRO1132.  
FN US2003032023-A1.  
PD 13-FEB-2003.  
Query Match 41.1%; Score 564.5; DB 6; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 806  
ID ABO17843 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
FN US2003032156-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 6; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 807  
ID ADA57425 standard; protein; 293 AA.  
DE Human secreted protein #257.  
FN WO2002102994-A2.  
PD 27-DEC-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 41.1%; Score 564.5; DB 6; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 808

ID ADA56974 standard; protein; 293 AA.  
DE Human secreted protein #257.  
PN WO2002102994-A2.  
PD 27-DEC-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 41.1%; Score 564.5; DB 6; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 809  
ID ADA57427 standard; protein; 293 AA.  
DE Human secreted protein #257.  
PN WO2002102994-A2.  
PD 27-DEC-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 41.1%; Score 564.5; DB 6; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 810  
ID ADA57428 standard; protein; 293 AA.  
DE Human secreted protein #257.  
PN WO2002102994-A2.  
PD 27-DEC-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 41.1%; Score 564.5; DB 6; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 811  
ID ABU60573 standard; protein; 293 AA.  
DE Human secreted/transmembrane protein, #130.  
PN US2002160384-A1.  
PD 31-OCT-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 6; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 812  
ID ABU13955 standard; protein; 293 AA.  
DE Human PRO1132 polypeptide.  
PN US2002103125-A1.  
PD 01-AUG-2002.  
PA (GETH ) GENENTECH LTD.  
Query Match 41.1%; Score 564.5; DB 6; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 813  
ID ABU81097 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003004311-A1.  
PD 02-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 6; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 814  
ID ABU72540 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003003531-A1.  
PD 02-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 6; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 815  
ID ABU66797 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003036180-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 6; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 816  
ID ADA41303 standard; protein; 293 AA.  
DE Human secreted protein.  
PN WO2002102993-A2.  
PD 27-DEC-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 41.1%; Score 564.5; DB 6; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 817  
ID ADA41305 standard; protein; 293 AA.  
DE Human secreted protein.  
PN WO2002102993-A2.  
PD 27-DEC-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 41.1%; Score 564.5; DB 6; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 818  
ID ADA40825 standard; protein; 293 AA.  
DE Human secreted protein.  
PN WO2002102993-A2.  
PD 27-DEC-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 41.1%; Score 564.5; DB 6; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 819  
ID ADA41306 standard; protein; 293 AA.  
DE Human secreted protein.  
PN WO2002102993-A2.  
PD 27-DEC-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 41.1%; Score 564.5; DB 6; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 820  
ID ABU59878 standard; protein; 293 AA.  
DE Novel secreted and transmembrane protein PRO1132.  
PN US2003017563-A1.  
PD 23-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 6; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 821  
ID ABU59289 standard; protein; 293 AA.  
DE Human secreted/transmembrane protein, #130.  
PN US2003027162-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 6; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 822  
ID ABO25986 standard; protein; 293 AA.  
DE Human PRO1132 polypeptide.  
PN US2002127576-A1.  
PD 12-SEP-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 6; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 823  
ID ABO25068 standard; protein; 293 AA.  
DE Human secreted/transmembrane protein (PRO) #228.  
PN US2003036179-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 6; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 824  
ID ABU58995 standard; protein; 293 AA.  
DE Human secreted/transmembrane protein, #130.  
PN US2002142961-A1.  
PD 03-OCT-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 6; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 825  
ID ABU92373 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003022187-A1.  
PD 30-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 6; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 826  
ID ABU59438 standard; protein; 293 AA.  
DE Novel human secreted or transmembrane protein PRO1346.  
PN US2003027985-A1.  
PD 06-FEB-2003.

Query Match 41.1%; Score 564.5; DB 6; Length 293;  
 Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
 RESULT 827  
 ID ABU67073 standard; protein; 293 AA.  
 DE Human secreted/transmembrane, PRO, protein SEQ ID 456.  
 PN US2003032155-A1.  
 PD 13-FEB-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 41.1%; Score 564.5; DB 6; Length 293;  
 Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
 RESULT 828  
 ID ABU92204 standard; protein; 293 AA.  
 DE Novel human secreted and transmembrane protein PRO1132.  
 PN US2003017476-A1.  
 PD 23-JAN-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 41.1%; Score 564.5; DB 6; Length 293;  
 Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
 RESULT 829  
 ID ABU10910 standard; protein; 293 AA.  
 DE Human PRO polypeptide #96.  
 PN US2002123463-A1.  
 PD 05-SEP-2002.  
 PA (GETH ) GENENTECH INC.  
 Query Match 41.1%; Score 564.5; DB 6; Length 293;  
 Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
 RESULT 830  
 ID ABU81662 standard; protein; 293 AA.  
 DE Novel human secreted and transmembrane protein PRO1132.  
 PN US2002177164-A1.  
 PD 28-NOV-2002.  
 PA (GETH ) GENENTECH INC.  
 Query Match 41.1%; Score 564.5; DB 6; Length 293;  
 Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
 RESULT 831  
 ID ABU88601 standard; protein; 293 AA.  
 DE Human secreted and transmembrane polypeptide PRO1132.  
 PN US2002197615-A1.  
 PD 26-DEC-2002.  
 PA (GETH ) GENENTECH INC.  
 Query Match 41.1%; Score 564.5; DB 6; Length 293;  
 Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
 RESULT 832  
 ID ABO34115 standard; protein; 293 AA.  
 DE Human PRO1132 polypeptide.  
 PN US2003017981-A1.  
 PD 23-JAN-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 41.1%; Score 564.5; DB 6; Length 293;  
 Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
 RESULT 833  
 ID ADA45975 standard; protein; 293 AA.  
 DE Novel human secreted and transmembrane protein PRO1132.  
 PN US2003022328-A1.  
 PD 30-JAN-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 41.1%; Score 564.5; DB 6; Length 293;  
 Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
 RESULT 834  
 ID ADA76406 standard; protein; 293 AA.  
 DE Human PRO polypeptide #228.  
 PN US2003073212-A1.  
 PD 17-APR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 41.1%; Score 564.5; DB 6; Length 293;  
 Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
 RESULT 835  
 ID ADA19056 standard; protein; 293 AA.  
 DE Human PRO polypeptide #228.  
 PN US2003054517-A1.  
 PD 20-MAR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 41.1%; Score 564.5; DB 6; Length 293;  
 Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
 RESULT 836

ID ADA61679 standard; protein; 293 AA.  
 DE Homo sapiens.  
 PN US2003049816-A1.  
 PD 13-MAR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 41.1%; Score 564.5; DB 6; Length 293;  
 Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
 RESULT 837  
 ID ADB19464 standard; protein; 293 AA.  
 DE Novel human secreted and transmembrane protein PRO1132.  
 PN US2003068796-A1.  
 PD 10-APR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 41.1%; Score 564.5; DB 6; Length 293;  
 Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
 RESULT 838  
 ID ADB28005 standard; protein; 293 AA.  
 DE Human PRO polypeptide #228.  
 PN US2003082704-A1.  
 PD 01-MAY-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 41.1%; Score 564.5; DB 6; Length 293;  
 Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
 RESULT 839  
 ID ADA86484 standard; protein; 293 AA.  
 DE Novel human secreted and transmembrane protein PRO1132.  
 PN US2003082711-A1.  
 PD 01-MAY-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 41.1%; Score 564.5; DB 6; Length 293;  
 Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
 RESULT 840  
 ID ADB16048 standard; protein; 293 AA.  
 DE Human PRO polypeptide #228.  
 PN US2003087350-A1.  
 PD 08-MAY-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 41.1%; Score 564.5; DB 6; Length 293;  
 Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
 RESULT 841  
 ID ADA37820 standard; protein; 293 AA.  
 DE Human secreted/transmembrane protein PRO1132.  
 PN US200308297-A1.  
 PD 09-JAN-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 41.1%; Score 564.5; DB 6; Length 293;  
 Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
 RESULT 842  
 ID ADA47834 standard; protein; 293 AA.  
 DE Human PRO polypeptide #228.  
 PN US2003073215-A1.  
 PD 17-APR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 41.1%; Score 564.5; DB 6; Length 293;  
 Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
 RESULT 843  
 ID ADA21506 standard; protein; 293 AA.  
 DE Human secreted/transmembrane polypeptide PRO1132.  
 PN US2003054404-A1.  
 PD 20-MAR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 41.1%; Score 564.5; DB 6; Length 293;  
 Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
 RESULT 844  
 ID ADA10293 standard; protein; 293 AA.  
 DE Human secreted/transmembrane protein, PRO1132.  
 PN US2003059831-A1.  
 PD 27-MAR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 41.1%; Score 564.5; DB 6; Length 293;  
 Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
 RESULT 845  
 ID ADA67629 standard; protein; 293 AA.  
 DE Human PRO polypeptide #228.  
 PN US2003068795-A1.

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PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 6; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 846
ID ADB30636 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003068794-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 6; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 847
ID ADA85932 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003082693-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 6; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 848
ID ADA17837 standard; protein; 293 AA.
DE Human PRO1132 polypeptide.
PN US2003054987-A1.
PD 20-MAR-2003.
Query Match 41.1%; Score 564.5; DB 6; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 849
ID ADA97144 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003082705-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 6; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 850
ID ADA79448 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003082763-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 6; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 851
ID ADA87587 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003087345-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 6; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 852
ID ADB16789 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003087349-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 6; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 853
ID ADA27945 standard; protein; 293 AA.
DE Human secreted/transmembrane protein PRO1132.
PN US2003054359-A1.
PD 20-MAR-2003.
Query Match 41.1%; Score 564.5; DB 6; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 854
ID ADA91881 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003082694-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 6; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 855
ID ADB14944 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003087351-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 6; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 856
ID ADB18905 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003073211-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 6; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 857
ID ADA94120 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003077722-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 6; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 858
ID ADB20016 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003082691-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 6; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 859
ID ADB13328 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003082710-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 6; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 860
ID ABO43376 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003044945-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 6; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 861
ID ADA94525 standard; protein; 293 AA.
DE Human secreted/transmembrane protein PRO1132.
PN US2003059832-A1.
PD 27-MAR-2003.
Query Match 41.1%; Score 564.5; DB 6; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 862
ID ADA74582 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003068798-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 6; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 863
ID ADB24815 standard; protein; 293 AA.
DE Human PRO polypeptide SEQ ID NO 456.
PN US2003077713-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 6; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 864
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ID ADA82339 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003082701-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 6; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 865  
ID ADA75302 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003073216-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 6; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 866  
ID ADA85380 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003082695-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 6; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 867  
ID ADA84828 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003082708-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 6; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 868  
ID ADB30084 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003073214-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 6; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 869  
ID ADA80612 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003082761-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 6; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 870  
ID ADA75854 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003082703-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 6; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 871  
ID ADA38750 standard; protein; 293 AA.  
DE Human secreted/transmembrane protein PRO1132.  
PN US2003059780-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 6; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 872  
ID ADA47079 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003073210-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 6; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 873  
ID ADB25375 standard; protein; 293 AA.  
DE Human PRO polypeptide SEQ ID NO 456.

PN US2003077715-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 6; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 874  
ID ADA93551 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003077721-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 6; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 875  
ID ADB26901 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003092147-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 6; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 876  
ID ADB31188 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003096386-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 6; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 877  
ID ADA92871 standard; protein; 293 AA.  
DE Human secreted/transmembrane protein PRO1132.  
PN US2003060407-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 6; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 878  
ID ADA61116 standard; protein; 293 AA.  
DE Homo sapiens.  
PN US2003049817-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 6; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 879  
ID ADB24263 standard; protein; 293 AA.  
DE Human PRO polypeptide SEQ ID NO 456.  
PN US2003077714-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 6; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 880  
ID ADA96592 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003082690-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 6; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 881  
ID ADA81164 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003082702-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 6; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 882  
ID ADA96040 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003082759-A1.  
PD 01-MAY-2003.

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PA (GETH ) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 6; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 883
ID ADB26349 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003082760-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 6; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 884
ID ADB21834 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003082765-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 6; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 885
ID ADA77613 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003068797-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 886
ID ADB18353 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003077710-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 887
ID ADA87036 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003082709-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 888
ID ADA88139 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003082700-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 889
ID ADA46527 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003054516-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 890
ID ADB28557 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003082699-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 891
ID ADB29109 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003082706-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 892
ID ABO53201 standard; protein; 293 AA.
DE Human secreted/transmembrane protein PRO1132.
PN US2003044806-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 893
ID ADA77061 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003059909-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 894
ID ADA22432 standard; protein; 293 AA.
DE Human secreted/transmembrane polypeptide PRO1132.
PN US2003040473-A1.
PD 27-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 895
ID ADA86691 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003073213-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 896
ID ADA97696 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003082686-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 897
ID ADB27453 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003022239-A1.
PD 30-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 898
ID ADB22386 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003087344-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 899
ID ABO22571 standard; protein; 293 AA.
DE Human secreted/transmembrane protein PRO1132.
PN US2003017982-A1.
PD 23-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 900
ID ADA06598 standard; protein; 293 AA.
DE Human secreted/transmembrane PRO polypeptide #96.
PN US2003049638-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 901
ID ADA39291 standard; protein; 293 AA.
DE Human secreted/transmembrane protein PRO1132.
PN US2003059782-A1.
PD 27-MAR-2003.
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Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 902  
ID ADA67077 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003068793-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 903  
ID AD822938 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003077711-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 904  
ID AD823711 standard; protein; 293 AA.  
DE Human PRO polypeptide SEQ ID NO 456.  
PN US2003077712-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 905  
ID ADA92433 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003082712-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 906  
ID AD815496 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003087352-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 907  
ID ADB38748 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003082766-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 908  
ID ADB96317 standard; protein; 293 AA.  
DE Human PRO polypeptide #96.  
PN US2003054403-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 909  
ID ADB38196 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003087347-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 910  
ID ADB66668 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003082689-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;

RESULT 911  
ID ADB89748 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003082698-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 912  
ID ADB90480 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003082762-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 913  
ID ADB80490 standard; protein; 293 AA.  
DE Ovarian cancer-associated protein #27.  
PN WO2002102235-A2.  
PD 27-DEC-2002.  
PA (EOSB-) EOS BIOTECHNOLOGY INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 914  
ID ADB39581 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003082764-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 915  
ID ADB47204 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003082687-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 916  
ID ADB86811 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003082697-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 917  
ID ADB77416 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003082696-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 918  
ID ADB34573 standard; protein; 293 AA.  
DE Human PRO polypeptide SEQ ID NO 456.  
PN US2003077717-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 919  
ID ADB5677 standard; protein; 293 AA.  
DE Human PRO polypeptide SEQ ID NO 456.  
PN US2003077719-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 920

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ID ADB34021 standard; protein; 293 AA.
DE Human PRO polypeptide SEQ ID NO 456.
PN US2003077716-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match 41.1%; Score 564.5; DB 7; Length 293;
  Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 921
ID ADB35125 standard; protein; 293 AA.
DE Human PRO polypeptide SEQ ID NO 456.
PN US2003077718-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match 41.1%; Score 564.5; DB 7; Length 293;
  Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 922
ID ADB36229 standard; protein; 293 AA.
DE Human PRO polypeptide SEQ ID NO 456.
PN US2003077720-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match 41.1%; Score 564.5; DB 7; Length 293;
  Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 923
ID ADB46624 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003082692-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match 41.1%; Score 564.5; DB 7; Length 293;
  Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 924
ID ADC57789 standard; protein; 293 AA.
DE Human PRO polypeptide #96.
PN US2003027754-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
  Query Match 41.1%; Score 564.5; DB 7; Length 293;
  Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 925
ID ADC55153 standard; protein; 293 AA.
DE Human PRO polypeptide #96.
PN US2003045463-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
  Query Match 41.1%; Score 564.5; DB 7; Length 293;
  Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 926
ID ADC12020 standard; protein; 293 AA.
DE Human secreted/transmembrane protein PRO1132.
PN US2003049681-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
  Query Match 41.1%; Score 564.5; DB 7; Length 293;
  Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 927
ID ADC56442 standard; protein; 293 AA.
DE Human PRO polypeptide #96.
PN US2003064375-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match 41.1%; Score 564.5; DB 7; Length 293;
  Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 928
ID ADC07497 standard; protein; 293 AA.
DE Human secreted/transmembrane protein PRO1132.
PN US2003068647-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match 41.1%; Score 564.5; DB 7; Length 293;
  Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 929
ID ADC11487 standard; protein; 293 AA.
DE Human secreted/transmembrane protein PRO1132.
PN US2003069403-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match 41.1%; Score 564.5; DB 7; Length 293;
  Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 930
ID ADC50497 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003092106-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match 41.1%; Score 564.5; DB 7; Length 293;
  Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 931
ID ADC72044 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003092107-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match 41.1%; Score 564.5; DB 7; Length 293;
  Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 932
ID ADC60023 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003092105-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match 41.1%; Score 564.5; DB 7; Length 293;
  Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 933
ID ADC53030 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein Seq ID456.
PN US2003087365-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match 41.1%; Score 564.5; DB 7; Length 293;
  Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 934
ID ADC57384 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein Seq ID456.
PN US2003087366-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match 41.1%; Score 564.5; DB 7; Length 293;
  Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 935
ID ADC60575 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003087367-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match 41.1%; Score 564.5; DB 7; Length 293;
  Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 936
ID ADC51050 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003087361-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match 41.1%; Score 564.5; DB 7; Length 293;
  Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 937
ID ADC65577 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003087362-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match 41.1%; Score 564.5; DB 7; Length 293;
  Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 938
ID ADC54675 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein Seq ID456.
PN US2003087363-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match 41.1%; Score 564.5; DB 7; Length 293;
  Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 939
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ID ADC53636 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein Seq ID456.  
PN US2003087364-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 940  
ID ADC59159 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein Seq ID456.  
PN US2003087359-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 941  
ID ADC56037 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein Seq ID456.  
PN US2003087360-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 942  
ID ADC58607 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein Seq ID456.  
PN US2003087346-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 943  
ID ADC14609 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003082546-A1.  
PD 01-MAY-2003.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 944  
ID ADP08141 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003068623-A1.  
PD 10-APR-2003.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 945  
ID ADP03281 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003092104-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 946  
ID ADC90273 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003087348-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 947  
ID ADC81966 standard; protein; 293 AA.  
DE Human PRO polypeptide #96.  
PN US2003083461-A1.  
PD 01-MAY-2003.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 948  
ID ADC69692 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003194770-A1.  
PD 16-OCT-2003.

PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 949  
ID ADC48581 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003194773-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 950  
ID ADD10110 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003194776-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 951  
ID ADP07608 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2002193299-A1.  
PD 19-DEC-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 952  
ID ADP04685 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003087354-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 953  
ID ADC82499 standard; protein; 293 AA.  
DE Human PRO polypeptide #96.  
PN US2003059833-A1.  
PD 27-MAR-2003.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 954  
ID ADC80641 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003092103-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 955  
ID ADD11148 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003194774-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 956  
ID ADC48029 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003194771-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 957  
ID ADD08679 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003073090-A1.  
PD 17-APR-2003.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;

[illegible]

Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 977  
ID ADE32397 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
FN US2003194765-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 978  
ID ADE22329 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
FN US2003199056-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 979  
ID ADE42089 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
FN US2003194772-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 980  
ID ADE42089 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
FN US2003194772-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 981  
ID ADE17906 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
FN US2003199023-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 982  
ID ADD92038 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
FN US2003199053-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 983  
ID ADE33501 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
FN US2003194767-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 984  
ID ADE34053 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
FN US2003194791-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 985  
ID ADD80105 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
FN US2003207417-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;

Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 986  
ID ADD93142 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
FN US2003194768-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 987  
ID ADE19562 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
FN US2003199025-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 988  
ID ADE19010 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
FN US2003199026-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 989  
ID ADE43206 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
FN US2003199033-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 990  
ID ADD95995 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
FN US2003199059-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 991  
ID ADE22881 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
FN US2003199064-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 992  
ID ADD78999 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
FN US2003203429-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 993  
ID ADE26299 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
FN US2003087305-A1.  
PD 08-MAY-2003.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 994  
ID ADE32949 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
FN US2003194766-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 995

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ID ADE42641 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003199032-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match 41.1%; Score 564.5; DB 7; Length 293;
  Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 996
ID ADD80657 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003207418-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
  Query Match 41.1%; Score 564.5; DB 7; Length 293;
  Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 997
ID ADD89685 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003199028-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match 41.1%; Score 564.5; DB 7; Length 293;
  Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 998
ID ADE40969 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003199031-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match 41.1%; Score 564.5; DB 7; Length 293;
  Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 999
ID ADE04768 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003199034-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match 41.1%; Score 564.5; DB 7; Length 293;
  Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 1000
ID ADE92897 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003194777-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match 41.1%; Score 564.5; DB 7; Length 293;
  Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 1001
ID ADE67236 standard; protein; 293 AA.
DE Human PRO1132 amino acid sequence SEQ ID NO:309.
PN US2002198148-A1.
PD 26-DEC-2002.
PA (GETH ) GENENTECH INC.
  Query Match 41.1%; Score 564.5; DB 7; Length 293;
  Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 1002
ID ADG21606 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003207355-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
  Query Match 41.1%; Score 564.5; DB 7; Length 293;
  Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 1003
ID ADG23247 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003207384-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
  Query Match 41.1%; Score 564.5; DB 7; Length 293;
  Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 1004
ID ADF97582 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003207388-A1.
DE Human PRO polypeptide #228.
PN US2003207370-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
  Query Match 41.1%; Score 564.5; DB 7; Length 293;
  Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 1005
ID ADG80646 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003207373-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
  Query Match 41.1%; Score 564.5; DB 7; Length 293;
  Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 1006
ID ADG80094 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003207372-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
  Query Match 41.1%; Score 564.5; DB 7; Length 293;
  Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 1007
ID ADH55386 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003207381-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
  Query Match 41.1%; Score 564.5; DB 7; Length 293;
  Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 1008
ID ADH55938 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003207379-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
  Query Match 41.1%; Score 564.5; DB 7; Length 293;
  Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 1009
ID ADI35490 standard; protein; 293 AA.
DE Human PRO polypeptide #96.
PN US2003050457-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
  Query Match 41.1%; Score 564.5; DB 7; Length 293;
  Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 1010
ID ADI64157 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003207385-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
  Query Match 41.1%; Score 564.5; DB 7; Length 293;
  Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 1011
ID ADI65106 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003207386-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
  Query Match 41.1%; Score 564.5; DB 7; Length 293;
  Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 1012
ID ADI63605 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003207387-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
  Query Match 41.1%; Score 564.5; DB 7; Length 293;
  Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 1013
ID ADH82019 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003207388-A1.
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PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 1014  
ID ADH9982 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003049682-A1.  
PD 13-MAR-2003.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 1015  
ID ADH81467 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US200307377-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 1016  
ID ADM82636 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003087355-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 1017  
ID ADN16035 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003087353-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 1018  
ID ADN16664 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003087385-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 1019  
ID ADN39198 standard; protein; 293 AA.  
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:516.  
PN WO2003042661-A2.  
PD 22-MAY-2003.  
PA (EOSB-) EOS BIOTECHNOLOGY INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 1020  
ID ADN15483 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003087356-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 1021  
ID ADN14931 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003087357-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 1022  
ID ADC81193 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003092115-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 8; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 1023  
ID ADD76641 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003100087-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 8; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 1024  
ID ADD88005 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003092113-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 8; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 1025  
ID ADD86409 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003203440-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 8; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 1026  
ID ADE75857 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003211571-A1.  
PD 13-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 8; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 1027  
ID ADE23433 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003092108-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 8; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 1028  
ID ADE23985 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003092110-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 8; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 1029  
ID ADE24628 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003092111-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 8; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 1030  
ID ADD87453 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003203439-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 8; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 1031  
ID ADE89319 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003199062-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 8; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 1032  
ID ADC81193 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003092115-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.

Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 1032  
ID ADE18458 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003194794-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 8; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 1033  
ID ADE88767 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003199054-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 8; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 1034  
ID ADE94787 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003199027-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 8; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 1035  
ID ADE91198 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003199061-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 8; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 1036  
ID ADF35435 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003194760-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 8; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 1037  
ID ADE95339 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003199052-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 8; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 1038  
ID ADE93449 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003199060-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 8; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 1039  
ID ADF35030 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003199029-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 8; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 1040  
ID ADE92345 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003199051-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 8; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 1041  
ID ADE90646 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003199063-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 8; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 1042  
ID ADE91793 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003199058-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 8; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 1043  
ID ADE11685 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003228655-A1.  
PD 11-DEC-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 8; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 1044  
ID ADE902372 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003207352-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 8; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 1045  
ID ADE922158 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003207360-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 8; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 1046  
ID ADE92228 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003207376-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 8; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 1047  
ID ADF98134 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003207422-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 8; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 1048  
ID ADE924351 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003207426-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 8; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 1049  
ID ADF98705 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003208055-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 8; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 1050  
ID ADE903536 standard; protein; 293 AA.

DE Human PRO polypeptide #228.  
 PN US2003207351-A1.  
 PD 06-NOV-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 41.1%; Score 564.5; DB 8; Length 293;  
 Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
 RESULT 1051  
 ID ADF99257 standard; protein; 293 AA.  
 DE Human PRO polypeptide #228.  
 PN US2003207353-A1.  
 PD 06-NOV-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 41.1%; Score 564.5; DB 8; Length 293;  
 Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
 RESULT 1052  
 ID ADG16842 standard; protein; 293 AA.  
 DE Human PRO polypeptide #228.  
 PN US2003207359-A1.  
 PD 06-NOV-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 41.1%; Score 564.5; DB 8; Length 293;  
 Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
 RESULT 1053  
 ID ADG05301 standard; protein; 293 AA.  
 DE Human PRO polypeptide #228.  
 PN US2003207375-A1.  
 PD 06-NOV-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 41.1%; Score 564.5; DB 8; Length 293;  
 Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
 RESULT 1054  
 ID ADG19568 standard; protein; 293 AA.  
 DE Human PRO polypeptide #228.  
 PN US2003207425-A1.  
 PD 06-NOV-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 41.1%; Score 564.5; DB 8; Length 293;  
 Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
 RESULT 1055  
 ID ADG13405 standard; protein; 293 AA.  
 DE Human PRO polypeptide #228.  
 PN US2003207357-A1.  
 PD 06-NOV-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 41.1%; Score 564.5; DB 8; Length 293;  
 Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
 RESULT 1056  
 ID AG08462 standard; protein; 293 AA.  
 DE Novel human secreted and transmembrane protein PRO1132.  
 PN US2003207424-A1.  
 PD 06-NOV-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 41.1%; Score 564.5; DB 8; Length 293;  
 Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
 RESULT 1057  
 ID ADG15632 standard; protein; 293 AA.  
 DE Human PRO polypeptide #228.  
 PN US2003219885-A1.  
 PD 27-NOV-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 41.1%; Score 564.5; DB 8; Length 293;  
 Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
 RESULT 1058  
 ID ADF97030 standard; protein; 293 AA.  
 DE Human PRO polypeptide #228.  
 PN US2003207371-A1.  
 PD 06-NOV-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 41.1%; Score 564.5; DB 8; Length 293;  
 Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
 RESULT 1059  
 ID ADG06215 standard; protein; 293 AA.  
 DE Human PRO polypeptide #228.

PN US2003207374-A1.  
 PD 06-NOV-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 41.1%; Score 564.5; DB 8; Length 293;  
 Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
 RESULT 1060  
 ID ADG23799 standard; protein; 293 AA.  
 DE Novel human secreted and transmembrane protein PRO1132.  
 PN US2003207389-A1.  
 PD 06-NOV-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 41.1%; Score 564.5; DB 8; Length 293;  
 Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
 RESULT 1061  
 ID ADG04088 standard; protein; 293 AA.  
 DE Human PRO polypeptide #228.  
 PN US2003207423-A1.  
 PD 06-NOV-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 41.1%; Score 564.5; DB 8; Length 293;  
 Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
 RESULT 1062  
 ID ADG24989 standard; protein; 293 AA.  
 DE Novel human secreted and transmembrane protein PRO1132.  
 PN US2003207427-A1.  
 PD 06-NOV-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 41.1%; Score 564.5; DB 8; Length 293;  
 Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
 RESULT 1063  
 ID ADG07286 standard; protein; 293 AA.  
 DE Novel human secreted and transmembrane protein PRO1132.  
 PN US2003207350-A1.  
 PD 06-NOV-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 41.1%; Score 564.5; DB 8; Length 293;  
 Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
 RESULT 1064  
 ID ADG07838 standard; protein; 293 AA.  
 DE Novel human secreted and transmembrane protein PRO1132.  
 PN US2003207356-A1.  
 PD 06-NOV-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 41.1%; Score 564.5; DB 8; Length 293;  
 Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
 RESULT 1065  
 ID ADG53333 standard; protein; 293 AA.  
 DE Novel human secreted and transmembrane protein PRO1132.  
 PN US2003194778-A1.  
 PD 16-OCT-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 41.1%; Score 564.5; DB 8; Length 293;  
 Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
 RESULT 1066  
 ID ADG60997 standard; protein; 293 AA.  
 DE Novel human secreted and transmembrane protein PRO1132.  
 PN US2003207390-A1.  
 PD 06-NOV-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 41.1%; Score 564.5; DB 8; Length 293;  
 Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
 RESULT 1067  
 ID ADG62101 standard; protein; 293 AA.  
 DE Novel human secreted and transmembrane protein PRO1132.  
 PN US2003207428-A1.  
 PD 06-NOV-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 41.1%; Score 564.5; DB 8; Length 293;  
 Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
 RESULT 1068  
 ID ADG82302 standard; protein; 293 AA.  
 DE Human PRO polypeptide #228.  
 PN US2003207358-A1.

[illegible]

RESULT 1087  
ID ADG61549 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003207429-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 8; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 1088  
ID ADH20088 standard; protein; 293 AA.  
DE Human secreted/transmembrane protein PRO1132.  
PN US2003219856-A1.  
PD 27-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 8; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 1089  
ID ADH28636 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003022331-A1.  
PD 30-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 8; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 1090  
ID ADG54781 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003207367-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 8; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 1091  
ID ADG59821 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003207369-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 8; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 1092  
ID ADH1245 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003207361-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 8; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 1093  
ID ADG09988 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2004009548-A1.  
PD 15-JAN-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 8; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 1094  
ID ADH15459 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003207382-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 8; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 1095  
ID ADG09336 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2004009547-A1.  
PD 15-JAN-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 8; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 1096

ID ADH14791 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003207383-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 8; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 1097  
ID ADH18386 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003207349-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 8; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 1098  
ID ADJ63667 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2004039164-A1.  
PD 26-FEB-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 8; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 1099  
ID ADJ7562 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2004038336-A1.  
PD 26-FEB-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 8; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 1100  
ID ADJ65684 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2004038335-A1.  
PD 26-FEB-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 8; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 1101  
ID ADM27820 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2004048333-A1.  
PD 11-MAR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 8; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 1102  
ID ADK52481 standard; protein; 293 AA.  
DE Human kallikrein 5 protein.  
PN WO2004021008-A2.  
PD 11-MAR-2004.  
PA (MOUN ) MOUNT SINAI HOSPITAL.  
PA (YOUS ) YOUSEF G.  
Query Match 41.1%; Score 564.5; DB 8; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 1103  
ID ADM42544 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2004058424-A1.  
PD 25-MAR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 8; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 1104  
ID ADM28406 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2004077064-A1.  
PD 22-APR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 8; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 1105

ID ADI95888 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
FN US2003077659-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 45.3%; DB 8; Length 293;  
RESULT 1106  
ID ADI96440 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
FN US2003207354-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 45.3%; DB 8; Length 293;  
RESULT 1107  
ID ADR72621 standard; protein; 293 AA.  
DE Human renal cell carcinoma-related kallikrein 5 (hk5) protein.  
FN WO2004077060-A2.  
PD 10-SEP-2004.  
PA (MOUN ) MOUNT SINAI HOSPITAL.  
Query Match  
Best Local Similarity 41.1%; Score 564.5; DB 8; Length 293;  
RESULT 1108  
ID ADR72873 standard; protein; 293 AA.  
DE Human ovarian cancer-related tumour marker kallikrein 5 (hk5) protein.  
FN WO2004077060-A2.  
PD 10-SEP-2004.  
PA (MOUN ) MOUNT SINAI HOSPITAL.  
Query Match  
Best Local Similarity 41.1%; Score 564.5; DB 8; Length 293;  
RESULT 1109  
ID AAI14072 standard; protein; 322 AA.  
DE Human BS247 specific epitope.  
FN WO9922027-A1.  
PD 06-MAY-1999.  
PA (ABBO ) ABBOTT LAB.  
Query Match  
Best Local Similarity 41.1%; Score 564.5; DB 8; Length 293;  
RESULT 1110  
ID AAW07620 standard; protein; 276 AA.  
DE Human NES1 polypeptide.  
FN WO9639175-A1.  
PD 12-DEC-1996.  
PA (NEWB-) NEW ENGLAND MEDICAL CENT HOSPITALS INC.  
Query Match  
Best Local Similarity 41.0%; Score 564; DB 2; Length 276;  
RESULT 1111  
ID AAB21327 standard; protein; 276 AA.  
DE Human NES1.  
FN WO200053776-A2.  
PD 14-SEP-2000.  
PA (MOUN ) MOUNT SINAI HOSPITAL.  
Query Match  
Best Local Similarity 41.0%; Score 564; DB 3; Length 276;  
RESULT 1112  
ID ABG96356 standard; protein; 276 AA.  
DE Human ovarian cancer marker OV32.  
FN WO200271928-A2.  
PD 19-SEP-2002.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match  
Best Local Similarity 41.0%; Score 564; DB 5; Length 276;  
RESULT 1113  
ID AAU82729 standard; protein; 276 AA.  
DE Amino acid sequence of novel human protease #28.  
FN WO200200860-A2.  
PD 03-JAN-2002.  
PA (SUGE-) SUGEN INC.  
Query Match  
Best Local Similarity 41.0%; Score 564; DB 5; Length 276;  
RESULT 1114  
ID ADB80527 standard; protein; 276 AA.

DE Ovarian cancer-associated protein #46.  
FN WO2002102235-A2.  
PD 27-DEC-2002.  
PA (EOSB-) EOS BIOTECHNOLOGY INC.  
Query Match  
Best Local Similarity 41.0%; Score 564; DB 7; Length 276;  
RESULT 1115  
ID ADE40473 standard; protein; 276 AA.  
DE Human kallikrein 10 (gene ID 2045) protein.  
FN WO2003070883-A2.  
PD 28-AUG-2003.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match  
Best Local Similarity 41.0%; Score 564; DB 7; Length 276;  
RESULT 1116  
ID ADN39880 standard; protein; 276 AA.  
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:C250.  
FN WO2003042661-A2.  
PD 22-MAY-2003.  
PA (EOSB-) EOS BIOTECHNOLOGY INC.  
Query Match  
Best Local Similarity 41.0%; Score 564; DB 7; Length 276;  
RESULT 1117  
ID ADN04446 standard; protein; 276 AA.  
DE Antipsoriatic protein sequence #416.  
FN WO2004028479-A2.  
PD 08-APR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 41.0%; Score 564; DB 8; Length 276;  
RESULT 1118  
ID AQ89070 standard; protein; 276 AA.  
DE Human urological disorder related protein 2045 SEQ:22.  
FN WO2004065576-A2.  
PD 05-AUG-2004.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match  
Best Local Similarity 41.0%; Score 564; DB 8; Length 276;  
RESULT 1119  
ID ADR72628 standard; protein; 276 AA.  
DE Human renal cell carcinoma-related kallikrein 10 (hk10) protein.  
FN WO2004077060-A2.  
PD 10-SEP-2004.  
PA (MOUN ) MOUNT SINAI HOSPITAL.  
Query Match  
Best Local Similarity 41.0%; Score 564; DB 8; Length 276;  
RESULT 1120  
ID ADR72886 standard; protein; 276 AA.  
DE Human ovarian cancer-related tumour marker kallikrein 10 (hk10) protein.  
FN WO2004075713-A2.  
PD 10-SEP-2004.  
PA (MOUN ) MOUNT SINAI HOSPITAL.  
Query Match  
Best Local Similarity 41.0%; Score 564; DB 8; Length 276;  
RESULT 1121  
ID AAB21305 standard; protein; 237 AA.  
DE Human KLK-L6 protein #1.  
FN WO200053776-A2.  
PD 14-SEP-2000.  
PA (MOUN ) MOUNT SINAI HOSPITAL.  
Query Match  
Best Local Similarity 40.9%; Score 562; DB 3; Length 237;  
RESULT 1122  
ID AAB21299 standard; protein; 256 AA.  
DE Human KLK-L4 protein #1.  
FN WO200053776-A2.  
PD 14-SEP-2000.  
PA (MOUN ) MOUNT SINAI HOSPITAL.  
Query Match  
Best Local Similarity 40.9%; Score 561.5; DB 3; Length 256;  
RESULT 1123  
ID AAB21309 standard; protein; 287 AA.  
DE Human KLK-L2.

PN WO200053776-A2.  
PD 14-SEP-2000.  
PA (MOUN ) MOUNT SINAI HOSPITAL.  
Query Match 40.9%; Score 561.5; DB 3; Length 287;  
Best Local Similarity 46.1%; Pred. No. 2.5e-35;  
RESULT 1124  
ID ABB98259 standard; protein; 228 AA.  
DE Synthetic shortened trypsinogen SEQ ID NO 23.  
PN WO200261064-A2.  
PD 08-AUG-2002.  
PA (HOFF ) ROCHE DIAGNOSTICS GMBH.  
PA (HOFF ) HOFFMANN LA ROCHE & CO AG F.  
Query Match 40.8%; Score 561; DB 5; Length 228;  
Best Local Similarity 46.7%; Pred. No. 2.1e-35;  
RESULT 1125  
ID AAB21310 standard; protein; 239 AA.  
DE Human zyme.  
PN WO200053776-A2.  
PD 14-SEP-2000.  
PA (MOUN ) MOUNT SINAI HOSPITAL.  
Query Match 40.8%; Score 561; DB 3; Length 239;  
Best Local Similarity 46.7%; Pred. No. 2.3e-35;  
RESULT 1126  
ID AAR44532 standard; protein; 244 AA.  
DE Zyme APP-cleaving protease.  
PN EP576152-A1.  
PD 29-DEC-1993.  
PA (ELIL ) LILLY & CO ELI.  
Query Match 40.8%; Score 561; DB 2; Length 244;  
Best Local Similarity 46.7%; Pred. No. 2.3e-35;  
RESULT 1127  
ID AAW22985 standard; protein; 244 AA.  
DE Human serine protease 59 (SP59).  
PN JP09149790-A.  
PD 10-JUN-1997.  
PA (SUNR ) SUNTORY LTD.  
Query Match 40.8%; Score 561; DB 2; Length 244;  
Best Local Similarity 46.7%; Pred. No. 2.3e-35;  
RESULT 1128  
ID AAW51006 standard; protein; 244 AA.  
DE Protease M, a novel serine protease.  
PN WO9811238-A2.  
PD 19-MAR-1998.  
PA (DAND-) DANA FARBER CANCER INST INC.  
Query Match 40.8%; Score 561; DB 2; Length 244;  
Best Local Similarity 46.7%; Pred. No. 2.3e-35;  
RESULT 1129  
ID AAB21323 standard; protein; 244 AA.  
DE Human zyme.  
PN WO200053776-A2.  
PD 14-SEP-2000.  
PA (MOUN ) MOUNT SINAI HOSPITAL.  
Query Match 40.8%; Score 561; DB 3; Length 244;  
Best Local Similarity 46.7%; Pred. No. 2.3e-35;  
RESULT 1130  
ID AAE37572 standard; protein; 244 AA.  
DE Human 2047 protein.  
PN WO2003037258-A2.  
PD 08-MAY-2003.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 40.8%; Score 561; DB 6; Length 244;  
Best Local Similarity 46.7%; Pred. No. 2.3e-35;  
RESULT 1131  
ID ADB80567 standard; protein; 244 AA.  
DE Ovarian cancer-associated protein #66.  
PN WO2002102235-A2.  
PD 27-DEC-2002.  
PA (EOSB-) EOS BIOTECHNOLOGY INC.  
Query Match 40.8%; Score 561; DB 7; Length 244;  
Best Local Similarity 46.7%; Pred. No. 2.3e-35;  
RESULT 1132  
ID ADN39212 standard; protein; 244 AA.  
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:530.

PN WO2003042661-A2.  
PD 22-MAY-2003.  
PA (EOSB-) EOS BIOTECHNOLOGY INC.  
Query Match 40.8%; Score 561; DB 7; Length 244;  
Best Local Similarity 46.7%; Pred. No. 2.3e-35;  
RESULT 1133  
ID ADN4074 standard; protein; 244 AA.  
DE Antipsoiatric protein sequence #232.  
PN WO2004028479-A2.  
PD 08-APR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 40.8%; Score 561; DB 8; Length 244;  
Best Local Similarity 46.7%; Pred. No. 2.3e-35;  
RESULT 1134  
ID ADN29289 standard; protein; 244 AA.  
DE Human kallikrein 6 associated protein.  
PN US2004097452-A1.  
PD 20-MAY-2004.  
PA (ISIS-) ISIS PHARM INC.  
Query Match 40.8%; Score 561; DB 8; Length 244;  
Best Local Similarity 46.7%; Pred. No. 2.3e-35;  
RESULT 1135  
ID ADQ89076 standard; protein; 244 AA.  
DE Human urological disorder related protein 2047 SEQ:28.  
PN WO2004065576-A2.  
PD 05-AUG-2004.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 40.8%; Score 561; DB 8; Length 244;  
Best Local Similarity 46.7%; Pred. No. 2.3e-35;  
RESULT 1136  
ID ADR72624 standard; protein; 244 AA.  
DE Human renal cell carcinoma-related kallikrein 6 (hk6) protein.  
PN WO2004077060-A2.  
PD 10-SEP-2004.  
PA (MOUN ) MOUNT SINAI HOSPITAL.  
Query Match 40.8%; Score 561; DB 8; Length 244;  
Best Local Similarity 46.7%; Pred. No. 2.3e-35;  
RESULT 1137  
ID ADR72876 standard; protein; 244 AA.  
DE Human ovarian cancer-related tumour marker kallikrein 6 (hk6) protein.  
PN WO2004075713-A2.  
PD 10-SEP-2004.  
PA (MOUN ) MOUNT SINAI HOSPITAL.  
Query Match 40.8%; Score 561; DB 8; Length 244;  
Best Local Similarity 46.7%; Pred. No. 2.3e-35;  
RESULT 1138  
ID ABG96357 standard; protein; 244 AA.  
DE Human ovarian cancer marker OV33.  
PN WO200271928-A2.  
PD 19-SEP-2002.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 40.8%; Score 560; DB 5; Length 244;  
Best Local Similarity 46.9%; Pred. No. 2.7e-35;  
RESULT 1139  
ID AAB21297 standard; protein; 296 AA.  
DE Human KLK-L3 protein #1.  
PN WO200053776-A2.  
PD 14-SEP-2000.  
PA (MOUN ) MOUNT SINAI HOSPITAL.  
Query Match 40.5%; Score 557; DB 3; Length 296;  
Best Local Similarity 46.1%; Pred. No. 5.7e-35;  
RESULT 1140  
ID AAR67888 standard; protein; 253 AA.  
DE Human stratum corneum chymotrophic recombinant enzyme (SCCE).  
PN WO9500651-A1.  
PD 05-JAN-1995.  
PA (SYMB-) SYMBICOM AB.  
Query Match 40.4%; Score 555; DB 2; Length 253;  
Best Local Similarity 44.6%; Pred. No. 6.9e-35;  
RESULT 1141  
ID AAW05383 standard; protein; 253 AA.  
DE Human amyloid precursor protein protease.  
PN WO9631122-A1.

PD 10-OCT-1996.  
PA (ELIL ) LILLY & CO ELI.  
Query Match 40.4%; Score 555; DB 2; Length 253;  
Best Local Similarity 44.6%; Pred. No. 6.9e-35;  
RESULT 1142  
ID ABB84421 standard; peptide; 253 AA.  
DE Human SCCE protein N-terminal fragment SEQ ID 48.  
PN WO200262135-A2.  
PA (EGEL/) EGELRUD T.  
PA (HANS/) HANSSON L.  
Query Match 40.4%; Score 555; DB 5; Length 253;  
Best Local Similarity 44.6%; Pred. No. 6.9e-35;  
RESULT 1143  
ID ABB84406 standard; protein; 253 AA.  
DE Human SCCE protein.  
PN WO200262135-A2.  
PD 15-AUG-2002.  
PA (EGEL/) EGELRUD T.  
PA (HANS/) HANSSON L.  
Query Match 40.4%; Score 555; DB 5; Length 253;  
Best Local Similarity 44.6%; Pred. No. 6.9e-35;  
RESULT 1144  
ID AAU82740 standard; protein; 253 AA.  
DE Amino acid sequence of novel human protease #39.  
PN WO200200860-A2.  
PD 03-JAN-2002.  
PA (SUGE-) SUGEN INC.  
Query Match 40.4%; Score 555; DB 5; Length 253;  
Best Local Similarity 44.6%; Pred. No. 6.9e-35;  
RESULT 1145  
ID ABU07440 standard; protein; 253 AA.  
DE Protein differentially regulated in prostate cancer #43.  
PN WO200281638-A2.  
PD 17-OCT-2002.  
PA (ORIG-) ORIGENE TECHNOLOGIES INC.  
Query Match 40.4%; Score 555; DB 6; Length 253;  
Best Local Similarity 44.6%; Pred. No. 6.9e-35;  
RESULT 1146  
ID ABU07471 standard; protein; 253 AA.  
DE Protein differentially regulated in prostate cancer #74.  
PN WO200281638-A2.  
PD 17-OCT-2002.  
PA (ORIG-) ORIGENE TECHNOLOGIES INC.  
Query Match 40.4%; Score 555; DB 6; Length 253;  
Best Local Similarity 44.6%; Pred. No. 6.9e-35;  
RESULT 1147  
ID ABR58471 standard; protein; 253 AA.  
DE Human stratum corneum chymotryptic enzyme - ovarian cancer clone O1676P.  
PN WO2003029468-A1.  
PD 10-APR-2003.  
PA (CORI-) CORIXA CORP.  
Query Match 40.4%; Score 555; DB 6; Length 253;  
Best Local Similarity 44.6%; Pred. No. 6.9e-35;  
RESULT 1148  
ID ADB80484 standard; protein; 253 AA.  
DE Ovarian cancer-associated protein #24.  
PN WO2002102235-A2.  
PD 27-DEC-2002.  
PA (EOSB-) EOS BIOTECHNOLOGY INC.  
Query Match 40.4%; Score 555; DB 7; Length 253;  
Best Local Similarity 44.6%; Pred. No. 6.9e-35;  
RESULT 1149  
ID ADJ68833 standard; protein; 253 AA.  
DE Human heat mitochondrial protein as a therapeutic target SeqID639.  
PN WO2003087768-A2.  
PD 23-OCT-2003.  
PA (MITO-) MITOKOR.  
PA (BUCK-) BUCK INST AGE RES.  
Query Match 40.4%; Score 555; DB 7; Length 253;  
Best Local Similarity 44.6%; Pred. No. 6.9e-35;  
RESULT 1150  
ID ADN39180 standard; protein; 253 AA.

DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:498.  
PN WO2003042661-A2.  
PD 22-MAY-2003.  
PA (EOSB-) EOS BIOTECHNOLOGY INC.  
Query Match 40.4%; Score 555; DB 7; Length 253;  
Best Local Similarity 44.6%; Pred. No. 6.9e-35;  
RESULT 1151  
ID ADL06515 standard; protein; 253 AA.  
DE Human tumour-associated antigenic target (TAT) polypeptide #14.  
PN WO2004016225-A2.  
PD 26-FEB-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 40.4%; Score 555; DB 8; Length 253;  
Best Local Similarity 44.6%; Pred. No. 6.9e-35;  
RESULT 1152  
ID ADN04182 standard; protein; 253 AA.  
DE Antipsoriatic protein sequence #286.  
PN WO2004028479-A2.  
PD 08-APR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 40.4%; Score 555; DB 8; Length 253;  
Best Local Similarity 44.6%; Pred. No. 6.9e-35;  
RESULT 1153  
ID ADR72880 standard; protein; 253 AA.  
DE Human ovarian cancer-related tumour marker kallikrein 7 (hk7) protein.  
PN WO2004075713-A2.  
PD 10-SEP-2004.  
PA (MOUN ) MOUNT SINAI HOSPITAL.  
Query Match 40.4%; Score 555; DB 8; Length 253;  
Best Local Similarity 44.6%; Pred. No. 6.9e-35;  
RESULT 1154  
ID ADA05734 standard; protein; 252 AA.  
DE Human NOV18b protein SEQ ID NO:94.  
PN WO2003029424-A2.  
PD 10-APR-2003.  
PA (CURA-) CURAGEN CORP.  
Query Match 40.3%; Score 553.5; DB 6; Length 252;  
Best Local Similarity 46.6%; Pred. No. 9e-35;  
RESULT 1155  
ID AON62898 standard; protein; 252 AA.  
DE Human NOV18b.  
PN US2004038223-A1.  
PD 26-FEB-2004.  
PA (SMIT/) SMITHSON G.  
PA (MILL/) MILLET I.  
PA (PEYM/) PEYMAN J A.  
PA (KEKU/) KEKUDA R.  
PA (JUJU/) JU J.  
PA (LILL/) LI L.  
PA (GUOX/) GUO X.  
PA (PATT/) PATTURAJAN M.  
PA (SPYT/) SPYTEK K A.  
PA (EDIN/) EDINGER S R.  
PA (ELLE/) ELLERMAN K.  
PA (WALY/) WALYANKAR U M.  
PA (ORTT/) ORT T.  
PA (GORM/) GORMAN L.  
PA (ZERH/) ZERHUSEN B D.  
PA (ANDE/) ANDERSON D W.  
PA (ZHON/) ZHONG M.  
PA (CATT/) CATTERTON E.  
PA (JIWW/) JI W.  
PA (MILL/) MILLER C E.  
PA (RAST/) RASTELLI L.  
PA (STON/) STONE D J.  
PA (PENA/) PENA C E A.  
PA (SHEN/) SHENOY S G.  
PA (SHIM/) SHIMKETS R A.  
PA (ROTH/) ROTHENBERG M E.  
PA (LEAC/) LEACH M D.  
PA (AGEE/) AGE E M L.  
PA (BERG/) BERGHS C.  
PA (DIPJ/) DIPIPPO V A.



PA (EISE/) EISEN A.  
PA (GANG/) GANGOLLI E A.  
PA (RIEG/) RIEGER D K.  
PA (SPAD/) SPADERNA S K. 40.3%; Score 553.5; DB 8; Length 252;  
Query Match 46.6%; Pred. No. 9e-35;  
Best Local Similarity 46.6%; Pred. No. 9e-35;  
RESULT 1156  
ID AAY08025 standard; protein; 253 AA.  
DE Mouse protease-related protein (PVP).  
PN DE19736198-CI.  
PD 24-DEC-1998.  
PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.  
Query Match 40.3%; Score 553.5; DB 2; Length 253;  
Best Local Similarity 43.5%; Pred. No. 9e-35;  
RESULT 1157  
ID AUN62896 standard; protein; 250 AA.  
DE Human NOVI8a.  
PN US2004038223-A1.  
PD 26-FEB-2004.  
PA (SMIT/) SMITHSON G.  
PA (MILL/) MILLET I.  
PA (PEYM/) PEYMAN J A.  
PA (KEKU/) KEKUDA R.  
PA (JUUJ/) JU J.  
PA (LILL/) LI L.  
PA (GUOX/) GUO X.  
PA (PATT/) PATTURAJAN M.  
PA (SPYT/) SPYTEK K A.  
PA (EDIN/) EDINGER S R.  
PA (ELLE/) ELLERMAN K.  
PA (NALY/) MALYANKAR U M.  
PA (ORTT/) ORT T.  
PA (GORM/) GORMAN L.  
PA (ZERH/) ZERHUSEN B D.  
PA (ANDE/) ANDERSON D W.  
PA (ZHON/) ZHONG M.  
PA (CATT/) CATTERTON E.  
PA (JIWW/) JI W.  
PA (MILL/) MILLER C E.  
PA (RAST/) RASTELLI L.  
PA (STON/) STONE D J.  
PA (PENA/) PENNA C E A.  
PA (SHEN/) SHENOY S G.  
PA (SHIM/) SHIMKETS R A.  
PA (ROTH/) ROTHENBERG M E.  
PA (LEAC/) LEACH M D.  
PA (AGEE/) AGEE W L.  
PA (BERG/) BERGHS C.  
PA (DIPI/) DIPIPPO V A.  
PA (EISE/) EISEN A.  
PA (GANG/) GANGOLLI E A.  
PA (RIEG/) RIEGER D K.  
PA (SPAD/) SPADERNA S K.  
Query Match 40.2%; Score 553; DB 8; Length 250;  
Best Local Similarity 44.8%; Pred. No. 9.8e-35;  
RESULT 1158  
ID AAY77494 standard; protein; 229 AA.  
DE Bovine trypsinogen.  
PN WO200005384-A1.  
PD 03-FEB-2000.  
PA (PROD-) PRODIGENE INC.  
Query Match 40.2%; Score 552; DB 3; Length 229;  
Best Local Similarity 46.3%; Pred. No. 1.1e-34;  
RESULT 1159  
ID AAR53638 standard; protein; 230 AA.  
DE Bovine trypsinogen.  
PN EP597681-A1.  
PD 18-MAY-1994.  
PA (ELIL/) LILLY & CO ELI.  
Query Match 40.2%; Score 552; DB 2; Length 230;  
Best Local Similarity 47.5%; Pred. No. 1.1e-34;  
RESULT 1160  
ID AAY91926 standard; protein; 231 AA.

DE Recombinant trypsin.  
PN WO200017332-A1.  
PD 30-MAR-2000.  
PA (ELIL/) LILLY & CO ELI.  
Query Match 40.2%; Score 552; DB 3; Length 231;  
Best Local Similarity 46.3%; Pred. No. 1.1e-34;  
RESULT 1161  
ID AAB80953 standard; protein; 231 AA.  
DE Bovine met-phe-trypsinogen.  
PN WO200119970-A2.  
PD 22-MAR-2001.  
PA (ELIL/) LILLY & CO ELI.  
Query Match 40.2%; Score 552; DB 4; Length 231;  
Best Local Similarity 46.3%; Pred. No. 1.1e-34;  
RESULT 1162  
ID ADA05732 standard; protein; 250 AA.  
DE Human NOVI8a protein SEQ ID NO:92.  
PN WO2003029424-A2.  
PD 10-APR-2003.  
PA (CURA-) CURAGEN CORP.  
Query Match 40.2%; Score 552; DB 6; Length 250;  
Best Local Similarity 44.8%; Pred. No. 1.2e-34;  
RESULT 1163  
ID ABB84420 standard; peptide; 249 AA.  
DE Porcine SCCE protein N-terminal fragment SEQ ID 47.  
PN WO200262135-A2.  
PD 15-AUG-2002.  
PA (EGEL/) EGELRUD T.  
PA (HANS/) HANSSON L.  
Query Match 40.1%; Score 550.5; DB 5; Length 249;  
Best Local Similarity 46.7%; Pred. No. 1.5e-34;  
RESULT 1164  
ID AAB35701 standard; protein; 247 AA.  
DE Human trypsin HL amino acid sequence.  
PN JF2000253887-A.  
PD 19-SEP-2000.  
PA (TTPH-) TT PHARMA KK.  
Query Match 40.0%; Score 549.5; DB 3; Length 247;  
Best Local Similarity 44.0%; Pred. No. 1.8e-34;  
RESULT 1165  
ID AAU86677 standard; protein; 247 AA.  
DE Novel human connective tissue related polypeptide #243.  
PN WO200155343-A1.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 39.8%; Score 547.5; DB 4; Length 247;  
Best Local Similarity 46.1%; Pred. No. 2.6e-34;  
RESULT 1166  
ID AAU23752 standard; protein; 247 AA.  
DE Novel human enzyme polypeptide #838.  
PN WO200155301-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 39.8%; Score 547.5; DB 4; Length 247;  
Best Local Similarity 46.1%; Pred. No. 2.6e-34;  
RESULT 1167  
ID AAU17043 standard; protein; 247 AA.  
DE Human novel secreted protein, SEQ ID 284.  
PN WO200155441-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 39.8%; Score 547.5; DB 4; Length 247;  
Best Local Similarity 46.1%; Pred. No. 2.6e-34;  
RESULT 1168  
ID ADB60011 standard; protein; 247 AA.  
DE Connective tissue antigen (CTA) #243.  
PN US2003054375-A1.  
PD 20-MAR-2003.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 39.8%; Score 547.5; DB 7; Length 247;  
Best Local Similarity 46.1%; Pred. No. 2.6e-34;  
RESULT 1169  
ID AAW81767 standard; peptide; 223 AA.

DE Bovine TRYP peptide fragment.  
PN JP10287696-A.  
PD 27-OCT-1998.  
PA (IYAK-) IYAKU BUNSHI SEKKEI KENKYUSHO KK.  
Query Match 39.8%; Score 547; DB 2; Length 223;  
Best Local Similarity 46.1%; Pred. No. 2.5e-34;  
RESULT 1170  
ID AAY69973 standard; protein; 223 AA.  
DE TRYP protein.  
PN WO9962004-A1.  
PD 02-DEC-1999.  
PA (MEDI-) INST MEDICINAL MOLECULAR DESIGN INC.  
Query Match 39.8%; Score 547; DB 3; Length 223;  
Best Local Similarity 46.1%; Pred. No. 2.5e-34;  
RESULT 1171  
ID ABG31841 standard; protein; 223 AA.  
DE Example protein #3 used in three-dimensional structure analysis method.  
PN WO200257954-A1.  
PD 25-JUL-2002.  
PA (MITU) MITSUBISHI CHEM CORP.  
PA (UMEY) UMEYAMA H.  
Query Match 39.8%; Score 547; DB 5; Length 223;  
Best Local Similarity 46.1%; Pred. No. 2.5e-34;  
RESULT 1172  
ID ADC73287 standard; protein; 223 AA.  
DE Bovine 2PTC-E protein - SEQ ID 13.  
PN WO2003060765-A1.  
PD 24-JUL-2003.  
PA (AJIN) AJINOMOTO CO INC.  
PA (UMEY) UMEYAMA H.  
Query Match 39.8%; Score 547; DB 7; Length 223;  
Best Local Similarity 46.1%; Pred. No. 2.5e-34;  
RESULT 1173  
ID ADD35545 standard; protein; 223 AA.  
DE Cationic bovine trypsinogen TRY1.  
PN WO2003040093-A2.  
PD 15-MAY-2003.  
PA (FARB) BAYER AG.  
Query Match 39.8%; Score 547; DB 7; Length 223;  
Best Local Similarity 46.1%; Pred. No. 2.5e-34;  
RESULT 1174  
ID AAR53637 standard; protein; 224 AA.  
DE Bovine trypsin.  
PN EP597681-A1.  
PD 18-MAY-1994.  
PA (ELIL) LILLY & CO ELI.  
Query Match 39.8%; Score 547; DB 2; Length 224;  
Best Local Similarity 46.1%; Pred. No. 2.5e-34;  
RESULT 1175  
ID AAY91925 standard; protein; 233 AA.  
DE Trypsinogen analogue.  
PN WO200017332-A1.  
PD 30-MAR-2000.  
PA (ELIL) LILLY & CO ELI.  
Query Match 39.8%; Score 547; DB 3; Length 233;  
Best Local Similarity 46.1%; Pred. No. 2.6e-34;  
RESULT 1176  
ID ADI39734 standard; protein; 244 AA.  
DE Human protease M (prom) protein.  
PN US6642013-B1.  
PD 04-NOV-2003.  
PA (UVAR-) UNIV ARKANSAS MEDICAL SCI.  
Query Match 39.7%; Score 546; DB 8; Length 244;  
Best Local Similarity 45.8%; Pred. No. 3.3e-34;  
RESULT 1177  
ID ADI37158 standard; protein; 244 AA.  
DE Human protease m (Protm).  
PN US2003199010-A1.  
PD 23-OCT-2003.  
PA (UVAR-) UNIV ARKANSAS.  
Query Match 39.7%; Score 546; DB 8; Length 244;  
Best Local Similarity 45.8%; Pred. No. 3.3e-34;  
RESULT 1178  
ID AAY78974 standard; protein; 247 AA.  
DE Canine cationic trypsinogen amino acid sequence.  
PN WO200009739-A1.  
PD 24-FEB-2000.  
PA (FUJY) FUJII YAKUHIIN KOGYO KK.  
Query Match 39.7%; Score 546; DB 3; Length 247;  
Best Local Similarity 45.6%; Pred. No. 3.3e-34;  
RESULT 1179  
ID ADA05742 standard; protein; 247 AA.  
DE Human NOVI8f protein SEQ ID NO:102.  
PN WO2003029424-A2.  
PD 10-APR-2003.  
PA (CURA-) CURAGEN CORP.  
Query Match 39.7%; Score 546; DB 6; Length 247;  
Best Local Similarity 45.5%; Pred. No. 3.3e-34;  
RESULT 1180  
ID ADN62906 standard; protein; 247 AA.  
DE Human NOVI8f.  
PN US2004038223-A1.  
PD 26-FEB-2004.  
PA (SMIT) SMITHSON G.  
PA (MILL) MILLET I.  
PA (PEYM) PEYMAN J A.  
PA (KEKU) KEKUDA R.  
PA (JUJJ) JU J.  
PA (LILL) LI L.  
PA (GUOX) GUO X.  
PA (PATT) PATTURAJAN M.  
PA (SPYT) SPYTEK K A.  
PA (EDIN) EDINGER S R.  
PA (ELLE) ELLERMAN K.  
PA (MALY) MALYANKAR U M.  
PA (ORTT) ORT T.  
PA (GORM) GORMAN L.  
PA (ZERH) ZERHUSEN B D.  
PA (ANDE) ANDERSON D W.  
PA (ZHON) ZHONG M.  
PA (CATT) CATTERTON E.  
PA (JIWW) JI W.  
PA (MILL) MILLER C E.  
PA (RAST) RASTELLI L.  
PA (STON) STONE D J.  
PA (PENA) PENNA C E A.  
PA (SHEN) SHENOY S G.  
PA (SHIM) SHIMKETS R A.  
PA (ROTH) ROTHENBERG M E.  
PA (LEAC) LEACH M D.  
PA (AGEE) AGEY M L.  
PA (BERG) BERGHS C.  
PA (DIPI) DIPIPPO V A.  
PA (EISE) EISEN A.  
PA (GANG) GANGOLLI E A.  
PA (RIEG) RIEGER D K.  
PA (SPAD) SPADERNA S K.  
Query Match 39.7%; Score 546; DB 8; Length 247;  
Best Local Similarity 45.5%; Pred. No. 3.3e-34;  
RESULT 1181  
ID AAB98502 standard; protein; 225 AA.  
DE Human Stratum Corneum Chymotryptic Enzyme, SCCE, catalytic domain.  
PN WO200129056-A1.  
PD 26-APR-2001.  
PA (UVAR-) UNIV ARKANSAS.  
Query Match 39.7%; Score 545; DB 4; Length 225;  
Best Local Similarity 46.5%; Pred. No. 3.6e-34;  
RESULT 1182  
ID AAY78975 standard; protein; 246 AA.  
DE Canine anionic trypsinogen amino acid sequence.  
PN WO200009739-A1.  
PD 24-FEB-2000.  
PA (FUJY) FUJII YAKUHIIN KOGYO KK.  
Query Match 39.7%; Score 545; DB 3; Length 246;  
Best Local Similarity 44.2%; Pred. No. 4e-34;  
RESULT 1183

ID AAB21326 standard; protein; 257 AA.  
DE Human HSCCE.  
PN WO200053776-A2.  
PD 14-SEP-2000.  
PA (MOUN ) MOUNT SINAI HOSPITAL.  
Query Match 39.6%; Score 544; DB 3; Length 257;  
Best Local Similarity 44.1%; Pred. No. 5e-34;  
RESULT 1184  
ID AAW64260 standard; protein; 246 AA.  
DE Human amyloid beta-protein precursor inhibitor.  
PN WO9824886-A1.  
PD 11-JUN-1998.  
PA (BGHM ) BRIGHAM & WOMENS HOSPITAL.  
Query Match 39.5%; Score 543; DB 2; Length 246;  
Best Local Similarity 44.5%; Pred. No. 5.7e-34;  
RESULT 1185  
ID ADC73299 standard; protein; 220 AA.  
DE Stereostereorelated 2PFC\_E protein.  
PN WO2003060765-A1.  
PD 24-JUL-2003.  
PA (AJIN ) AJINOMOTO CO INC.  
PA (UMEX/) UMEYAMA H.  
Query Match 39.4%; Score 541; DB 7; Length 220;  
Best Local Similarity 46.8%; Pred. No. 7.2e-34;  
RESULT 1186  
ID ADC73301 standard; protein; 279 AA.  
DE Stereostereorelated 2PFC protein.  
PN WO2003060765-A1.  
PD 24-JUL-2003.  
PA (AJIN ) AJINOMOTO CO INC.  
PA (UMEX/) UMEYAMA H.  
Query Match 39.4%; Score 541; DB 7; Length 279;  
Best Local Similarity 46.8%; Pred. No. 9.2e-34;  
RESULT 1187  
ID AD116686 standard; protein; 259 AA.  
DE Human NOVX protein to treat human pathological conditions SeqID222.  
PN WO200268649-A2.  
PD 06-SEP-2002.  
PA (CURA-) CURAGEN CORP.  
Query Match 39.3%; Score 539.5; DB 5; Length 259;  
Best Local Similarity 44.4%; Pred. No. 1.1e-33;  
RESULT 1188  
ID ADN42340 standard; protein; 259 AA.  
DE Human novel proteinNOV 62.  
PN US2004033493-A1.  
PD 19-FEB-2004.  
PA (TCHE/) TCHERNEV V T.  
PA (SPYT/) SPYTEK K A.  
PA (ZERH/) ZERHUSEN B D.  
PA (PATT/) PATTURAJAN M.  
PA (SHIM/) SHIMKETS R A.  
PA (LILL/) LI L.  
PA (GANG/) GANGOLLI E A.  
PA (PADI/) PADIGARU M.  
PA (ANDE/) ANDERSON D W.  
PA (RAST/) RASTELLI L.  
PA (MILL/) MILLER C E.  
PA (GERL/) GERLACH V.  
PA (TRUP/) TRUPIER R J.  
PA (GUSE/) GUSEV V Y.  
PA (COLM/) COLMAN S D.  
PA (MOLE/) MOLENC A R.  
PA (PENA/) PENA C E A.  
PA (FURT/) FURTAK K.  
PA (GROS/) GROSSE W M.  
PA (ALSO/) ALSOBROOK J P.  
PA (LEPL/) LEFLEY D M.  
PA (RIEG/) RIEGER D K.  
PA (BURG/) BURGESS C E.  
Query Match 39.3%; Score 539.5; DB 8; Length 259;  
Best Local Similarity 44.4%; Pred. No. 1.1e-33;  
RESULT 1189  
ID ABB78122 standard; peptide; 223 AA.  
DE Amino acid sequence of trypsin.  
PN US2002072863-A1.  
PD 13-JUN-2002.  
PA (FUIT ) FUJITSU LTD.  
Query Match 39.2%; Score 538; DB 5; Length 223;  
Best Local Similarity 45.6%; Pred. No. 1.2e-33;  
RESULT 1190  
ID ABB83322 standard; protein; 223 AA.  
DE Partial trypsin sequence.  
PN US2002035434-A1.  
PD 21-MAR-2002.  
PA (FUIT ) FUJITSU LTD.  
Query Match 39.2%; Score 538; DB 5; Length 223;  
Best Local Similarity 45.6%; Pred. No. 1.2e-33;  
RESULT 1191  
ID ABB84419 standard; peptide; 243 AA.  
DE Bovine SCCE protein N-terminal fragment SEQ ID 46.  
PN WO200262135-A2.  
PD 15-AUG-2002.  
PA (EGEL/) EGELRUD T.  
PA (HANS/) HANSSON L.  
Query Match 38.7%; Score 531.5; DB 5; Length 243;  
Best Local Similarity 43.8%; Pred. No. 4.3e-33;  
RESULT 1192  
ID ABB04644 standard; protein; 240 AA.  
DE Engraulis japonicus trypsinogen (atry I) SEQ ID NO:1.  
PN JP2001269173-A.  
PD 02-OCT-2001.  
PA (NISE ) JAPAN TOBACCO INC.  
Query Match 38.2%; Score 525; DB 5; Length 240;  
Best Local Similarity 45.7%; Pred. No. 1.3e-32;  
RESULT 1193  
ID AAW64261 standard; protein; 232 AA.  
DE Kallikrein substrate binding site.  
PN WO9824886-A1.  
PD 11-JUN-1998.  
PA (BGHM ) BRIGHAM & WOMENS HOSPITAL.  
Query Match 38.1%; Score 524; DB 2; Length 232;  
Best Local Similarity 43.6%; Pred. No. 1.6e-32;  
RESULT 1194  
ID ABB84423 standard; peptide; 249 AA.  
DE Murine SCCE protein N-terminal fragment SEQ ID 50.  
PN WO200262135-A2.  
PD 15-AUG-2002.  
PA (EGEL/) EGELRUD T.  
PA (HANS/) HANSSON L.  
Query Match 38.0%; Score 521.5; DB 5; Length 249;  
Best Local Similarity 43.0%; Pred. No. 2.6e-32;  
RESULT 1195  
ID ABR96164 standard; protein; 261 AA.  
DE Human NOV13a protein SEQ ID NO:70.  
PN WO200290568-A2.  
PD 14-NOV-2002.  
PA (CURA-) CURAGEN CORP.  
Query Match 37.8%; Score 519.5; DB 6; Length 261;  
Best Local Similarity 40.0%; Pred. No. 3.9e-32;  
RESULT 1196  
ID ADL15205 standard; protein; 232 AA.  
DE Pancreatic kallikrein #1.  
PN CN1384199-A.  
PD 11-DEC-2002.  
PA (REMI-) REMIN HOSPITAL SHENZHEN CITY.  
Query Match 37.8%; Score 519; DB 7; Length 232;  
Best Local Similarity 44.5%; Pred. No. 3.8e-32;  
RESULT 1197  
ID ABG70276 standard; protein; 247 AA.  
DE Human Serine Protease TLSP-like protein.  
PN WO200255702-A2.  
PD 18-JUL-2002.  
PA (CURA-) CURAGEN CORP.  
Query Match 37.6%; Score 516; DB 5; Length 247;  
Best Local Similarity 42.5%; Pred. No. 6.9e-32;  
RESULT 1198

ID AAW94493 standard; protein; 268 AA.  
DE Human kallikrein.  
PN WO9842849-A1.  
PD 01-OCT-1998.  
PA (INCY-) INCYTE PHARM INC.  
Query Match 37.4%; Score 514; DB 2; Length 268;  
Best Local Similarity 46.4%; Pred. No. 1.1e-31;  
RESULT 1199  
ID ABO4645 standard; protein; 241 AA.  
DE Engraulis japonicus trypsinogen (arry II) SEQ ID NO:2.  
PN JP2001269173-A.  
PD 02-OCT-2001.  
PA (NISB ) JAPAN TOBACCO INC.  
Query Match 36.7%; Score 504; DB 5; Length 241;  
Best Local Similarity 45.9%; Pred. No. 5.6e-31;  
RESULT 1200  
ID AAU87693 standard; protein; 247 AA.  
DE Human pancreatic tumour protein #5.  
PN WO200212331-A2.  
PD 14-FEB-2002.  
PA (CORI-) CORIXA CORP.  
Query Match 36.5%; Score 501; DB 5; Length 247;  
Best Local Similarity 43.3%; Pred. No. 9.8e-31;  
RESULT 1201  
ID ADN04140 standard; protein; 247 AA.  
DE Antiporiatic protein sequence #265.  
PN WO2004028479-A2.  
PD 08-APR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 36.5%; Score 501; DB 8; Length 247;  
Best Local Similarity 43.3%; Pred. No. 9.8e-31;  
RESULT 1202  
ID AN99594 standard; protein; 247 AA.  
DE Novel human protein sequence #410.  
PN WO2004038003-A2.  
PD 06-MAY-2004.  
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.  
Query Match 36.5%; Score 501; DB 8; Length 247;  
Best Local Similarity 43.3%; Pred. No. 9.8e-31;  
RESULT 1203  
ID ADQ30589 standard; protein; 247 AA.  
DE Pancreas cancer marker - trypsin II precursor.  
PN WO2004055519-A2.  
PD 01-JUL-2004.  
PA (HOFF ) HOFMANN LA ROCHE & CO AG F.  
PA (SINO-) SINGENOMAX CO LTD CHINESE NAT HUMAN GEN.  
Query Match 36.5%; Score 501; DB 8; Length 247;  
Best Local Similarity 43.3%; Pred. No. 9.8e-31;  
RESULT 1204  
ID ABR41530 standard; protein; 261 AA.  
DE Human DTHP protein modification/maintenance protein.  
PN WO200297031-A2.  
PD 05-DEC-2002.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match 36.5%; Score 501; DB 6; Length 261;  
Best Local Similarity 43.3%; Pred. No. 1e-30;  
RESULT 1205  
ID ABO3862 standard; protein; 223 AA.  
DE Human neurosin amino acid sequence.  
PN WO200031284-A1.  
PD 02-JUN-2000.  
PA (FUSO ) FUSO PHARM IND LTD.  
Query Match 36.4%; Score 500; DB 3; Length 223;  
Best Local Similarity 43.5%; Pred. No. 1.1e-30;  
RESULT 1206  
ID AAB21294 standard; protein; 254 AA.  
DE Human KLIK-L1 protein #2.  
PN WO200053776-A2.  
PD 14-SEP-2000.  
PA (MOUN ) MOUNT SINAI HOSPITAL.  
Query Match 36.2%; Score 498; DB 3; Length 254;  
Best Local Similarity 43.1%; Pred. No. 1.7e-30;  
RESULT 1207  
ID AAM01174 standard; protein; 254 AA.  
DE Human prostate-specific amino acid sequence P703P.  
PN WO200151633-A2.  
PD 19-JUL-2001.  
PA (CORI-) CORIXA CORP.  
Query Match 36.2%; Score 498; DB 4; Length 254;  
Best Local Similarity 43.1%; Pred. No. 1.7e-30;  
RESULT 1208  
ID AAU69819 standard; protein; 254 AA.  
DE Human prostate CDNA encoded protein #27.  
PN WO200173032-A2.  
PD 04-OCT-2001.  
PA (CORI-) CORIXA CORP.  
Query Match 36.2%; Score 498; DB 4; Length 254;  
Best Local Similarity 43.1%; Pred. No. 1.7e-30;  
RESULT 1209  
ID AAG99059 standard; protein; 254 AA.  
DE Human prostate-specific amino acid of P703P.  
PN WO200134802-A2.  
PD 17-MAY-2001.  
PA (CORI-) CORIXA CORP.  
Query Match 36.2%; Score 498; DB 4; Length 254;  
Best Local Similarity 43.1%; Pred. No. 1.7e-30;  
RESULT 1210  
ID ABU71710 standard; protein; 254 AA.  
DE Prostate cancer specific antigen P703P #7.  
PN US2002192763-A1.  
PD 19-DEC-2002.  
PA (XUJ/) XU J.  
PA (DILL/) DILLON D C.  
PA (MITC/) MITCHAM J L.  
PA (HARL/) HARLOCKER S L.  
PA (JIAN/) JIANG Y.  
PA (KALO/) KALOS M D.  
PA (FANG/) FANGER G R.  
PA (RETT/) RETTER M W.  
PA (STOL/) STOLK J A.  
PA (DAYC/) DAY C H.  
PA (VEDV/) VEDVICK T S.  
PA (CART/) CARTER D.  
PA (LISX/) LI S X.  
PA (WANG/) WANG A.  
PA (SKEI/) SKEIKY Y A W.  
PA (HEPL/) HEPLER W T.  
PA (HEND/) HENDERSON R A.  
PA (HURA/) HURAL J.  
PA (MCNE/) MCNEILL P D.  
PA (HOUG/) HOUGHTON R L.  
PA (DBAS/) Y DE BASSOLS C V.  
PA (FOYT/) FOY T M.  
Query Match 36.2%; Score 498; DB 4; Length 254;  
Best Local Similarity 43.1%; Pred. No. 1.7e-30;  
RESULT 1211  
ID ABB95279 standard; protein; 254 AA.  
DE Human P703P putative full length protein SEQ ID NO 525.  
PN US2002022248-A1.  
PD 21-FEB-2002.  
PA (XUJ/) XU J.  
PA (DILL/) DILLON D C.  
PA (MITC/) MITCHAM J L.  
PA (HARL/) HARLOCKER S L.  
PA (JIAN/) JIANG Y.  
PA (KALO/) KALOS M D.  
PA (FANG/) FANGER G R.  
PA (RETT/) RETTER M W.  
PA (STOL/) STOLK J A.  
PA (DAYC/) DAY C H.  
PA (VEDV/) VEDVICK T S.  
PA (CART/) CARTER D.  
PA (LISX/) LI S X.  
PA (WANG/) WANG A.  
PA (SKEI/) SKEIKY Y A W.  
PA (HEPL/) HEPLER W T.

PA (HEND//) HENDERSON R A.  
 Query Match 36.2%; Score 498; DB 5; Length 254;  
 Best Local Similarity 43.1%; Pred. No. 1.7e-30;  
 RESULT 1212  
 ID ABP54360 standard; protein; 254 AA.  
 DE Human KLK4 protein SEQ ID NO:13.  
 PN WO20027243-A1.  
 PD 03-OCT-2002.  
 PA (UYQU-) UNIV QUEBENS LAND TECHNOLOGY.  
 Query Match 36.2%; Score 498; DB 6; Length 254;  
 Best Local Similarity 43.1%; Pred. No. 1.7e-30;  
 RESULT 1213  
 ID ABP54357 standard; protein; 254 AA.  
 DE Human KLK4 protein SEQ ID NO:6.  
 PN WO20027243-A1.  
 PD 03-OCT-2002.  
 PA (UYQU-) UNIV QUEBENS LAND TECHNOLOGY.  
 Query Match 36.2%; Score 498; DB 6; Length 254;  
 Best Local Similarity 43.1%; Pred. No. 1.7e-30;  
 RESULT 1214  
 ID ABR54391 standard; protein; 254 AA.  
 DE Prostate tumour specific protein sequence SEQ ID 525.  
 PN WO200289747-A2.  
 PD 14-NOV-2002.  
 PA (CORI-) CORIXA CORP.  
 Query Match 36.2%; Score 498; DB 6; Length 254;  
 Best Local Similarity 43.1%; Pred. No. 1.7e-30;  
 RESULT 1215  
 ID ABR54391 standard; protein; 254 AA.  
 DE Human prostate specific protein P703P.  
 PN US2003185830-A1.  
 PD 02-OCT-2003.  
 PA (CORI-) CORIXA CORP.  
 Query Match 36.2%; Score 498; DB 7; Length 254;  
 Best Local Similarity 43.1%; Pred. No. 1.7e-30;  
 RESULT 1216  
 ID ADG26391 standard; protein; 254 AA.  
 DE Human prostate specific polypeptide #60.  
 PN US2003157089-A1.  
 PD 21-AUG-2003.  
 PA (CORI-) CORIXA CORP.  
 Query Match 36.2%; Score 498; DB 7; Length 254;  
 Best Local Similarity 43.1%; Pred. No. 1.7e-30;  
 RESULT 1217  
 ID AAB74830 standard; protein; 1079 AA.  
 DE Prostate tumour antigen amino acid sequence for a fusion protein.  
 PN WO200125272-A2.  
 PD 12-APR-2001.  
 PA (CORI-) CORIXA CORP.  
 Query Match 36.2%; Score 498; DB 4; Length 1079;  
 Best Local Similarity 43.1%; Pred. No. 7.6e-30;  
 RESULT 1218  
 ID ABU71860 standard; protein; 1079 AA.  
 DE Prostate specific antigen fusion protein #2.  
 PN US2002192763-A1.  
 PD 19-DEC-2002.  
 PA (XUJ//) XU J.  
 PA (DILL//) DILLON D C.  
 PA (MITC//) MITCHAM J L.  
 PA (HARL//) HARLOCKER S L.  
 PA (JIAN//) JIANG Y.  
 PA (KALO//) KALOS M D.  
 PA (FANG//) FANGER G R.  
 PA (RETT//) RETTER M W.  
 PA (STOL//) STOLK J A.  
 PA (DAYC//) DAY C H.  
 PA (VEDV//) VEDVICK T S.  
 PA (CART//) CARTER D.  
 PA (LISX//) LI S X.  
 PA (WANG//) WANG A.  
 PA (SKEI//) SKEIKY Y A W.  
 PA (HEPL//) HEPLER W T.  
 PA (HEND//) HENDERSON R A.

PA (HURA//) HURAL J.  
 PA (MCNE//) MCNEILL P D.  
 PA (HOUG//) HOUGHTON R L.  
 PA (DBAS//) Y DE BASSOLS C V.  
 PA (FOYT//) FOY T M.  
 Query Match 36.2%; Score 498; DB 4; Length 1079;  
 Best Local Similarity 43.1%; Pred. No. 7.6e-30;  
 RESULT 1219  
 ID ADI17268 standard; protein; 230 AA.  
 DE Polypeptide homologous to a human NOVX domain SeqID 804.  
 PN WO200268649-A2.  
 PD 06-SEP-2002.  
 PA (CURA-) CURAGEN CORP.  
 Query Match 36.2%; Score 497.5; DB 5; Length 230;  
 Best Local Similarity 47.4%; Pred. No. 1.7e-30;  
 RESULT 1220  
 ID ADI17276 standard; protein; 230 AA.  
 DE Polypeptide homologous to a human NOVX domain SeqID 812.  
 PN WO200268649-A2.  
 PD 06-SEP-2002.  
 PA (CURA-) CURAGEN CORP.  
 Query Match 36.2%; Score 497.5; DB 5; Length 230;  
 Best Local Similarity 47.4%; Pred. No. 1.7e-30;  
 RESULT 1221  
 ID ADJ83075 standard; protein; 230 AA.  
 DE Trypsin-like serine protease protein - SEQ ID 66.  
 PN US2003170630-A1.  
 PD 11-SEP-2003.  
 PA (ALSO//) ALSOBROOK J P.  
 PA (TCHE//) TCHERNEV V T.  
 PA (LIUX//) LIU X.  
 PA (SPYT//) SPYTEK K A.  
 PA (ZERH//) ZERHUSEN B D.  
 PA (PATT//) PATTURAJAN M.  
 PA (LEPL//) LEPLEY D M.  
 PA (BURG//) BURGESS C E.  
 PA (SHIM//) SHIMKETS R A.  
 PA (GROS//) GROSSE W M.  
 PA (SZEK//) SZEKERES E S.  
 PA (VERN//) VERNET C A M.  
 PA (LILL//) LI L.  
 PA (CASM//) CASMAN S J.  
 PA (BOLD//) BOLDOG F L.  
 PA (GORM//) GORMAN L.  
 PA (GANG//) GANGOLLI E A.  
 PA (FERN//) FERNANDES E R.  
 PA (RIEG//) RIEGER D K.  
 PA (EDIN//) EDINGER S R.  
 PA (GUNT//) GUNTHER E.  
 PA (MILL//) MILLET I.  
 PA (SCIO//) SCIORE P.  
 PA (ELLE//) ELLERMAN K.  
 PA (MACD//) MACDOUGALL J R.  
 PA (SMIT//) SMITHSON G.  
 Query Match 36.2%; Score 497.5; DB 7; Length 230;  
 Best Local Similarity 47.4%; Pred. No. 1.7e-30;  
 RESULT 1222  
 ID ADL27345 standard; peptide; 280 AA.  
 DE Amino acid sequence of trypsinogen.  
 PN WO2004019878-A2.  
 PD 11-MAR-2004.  
 PA (COMP-) COMPOUND THERAPEUTICS INC.  
 PA (AFEY//) AFEYAN N B.  
 Query Match 36.2%; Score 497.5; DB 8; Length 280;  
 Best Local Similarity 42.7%; Pred. No. 2.1e-30;  
 RESULT 1223  
 ID ADL27346 standard; peptide; 461 AA.  
 DE Amino acid sequence of trypsinogen-0aa-sp55.  
 PN WO2004019878-A2.  
 PD 11-MAR-2004.  
 PA (COMP-) COMPOUND THERAPEUTICS INC.  
 PA (AFEY//) AFEYAN N B.  
 Query Match 36.2%; Score 497.5; DB 8; Length 461;

Best Local Similarity 42.7%; Pred. No. 3.5e-30;  
RESULT 1224  
ID ADL27347 standard; peptide; 464 AA.  
DE Amino acid sequence of trypsinogen-3aa-sp55.  
PN WO2004019878-A2.  
PD 11-MAR-2004.  
PA (COMP-) COMPOUND THERAPEUTICS INC.  
PA (AFEPY/) AFEYAN N B. 36.2%; Score 497.5; DB 8; Length 464;  
Query Match  
Best Local Similarity 42.7%; Pred. No. 3.5e-30;  
RESULT 1225  
ID ADL27348 standard; peptide; 485 AA.  
DE Amino acid sequence of trypsinogen-20aa-sp55.  
PN WO2004019878-A2.  
PD 11-MAR-2004.  
PA (COMP-) COMPOUND THERAPEUTICS INC.  
PA (AFEPY/) AFEYAN N B. 36.2%; Score 497.5; DB 8; Length 485;  
Query Match  
Best Local Similarity 42.7%; Pred. No. 3.6e-30;  
RESULT 1226  
ID AAB21307 standard; protein; 249 AA.  
DE Human prostate.  
PN WO200053776-A2.  
PD 14-SEP-2000.  
PA (MOUN) MOUNT SINAI HOSPITAL.  
Query Match  
Best Local Similarity 43.1%; Pred. No. 2e-30;  
RESULT 1227  
ID AAB21320 standard; protein; 254 AA.  
DE Human prostate.  
PN WO200053776-A2.  
PD 14-SEP-2000.  
PA (MOUN) MOUNT SINAI HOSPITAL.  
Query Match  
Best Local Similarity 43.1%; Pred. No. 2.1e-30;  
RESULT 1228  
ID AAY72525 standard; protein; 254 AA.  
DE Human prostate antigen #3.  
PN WO200104143-A2.  
PD 18-JAN-2001.  
PA (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.  
PA (CORI-) CORIXA CORP. 36.2%; Score 497; DB 4; Length 254;  
Query Match  
Best Local Similarity 43.1%; Pred. No. 2.1e-30;  
RESULT 1229  
ID AAU74901 standard; protein; 254 AA.  
DE Protein sequence of prostate homologue #3.  
PN WO200200708-A2.  
PD 03-JAN-2002.  
PA (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.  
Query Match  
Best Local Similarity 43.1%; Pred. No. 2.1e-30;  
RESULT 1230  
ID AAU74932 standard; protein; 254 AA.  
DE Amino acid sequence of prostate protein fragment #3.  
PN WO200200867-A1.  
PD 03-JAN-2002.  
PA (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.  
Query Match  
Best Local Similarity 43.1%; Pred. No. 2.1e-30;  
RESULT 1231  
ID AAW60592 standard; protein; 248 AA.  
DE Human prostate-specific kallikrein (HPSK) protein.  
PN WO9820117-A1.  
PD 14-MAY-1998.  
PA (INCY-) INCYTE PHARM INC. 36.1%; Score 496.5; DB 2; Length 248;  
Query Match  
Best Local Similarity 43.4%; Pred. No. 2.2e-30;  
RESULT 1232  
ID AAY72524 standard; protein; 248 AA.  
DE Human prostate antigen #2.  
PN WO200104143-A2.  
PD 18-JAN-2001.  
PA (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.  
PA (CORI-) CORIXA CORP. 36.1%; Score 496.5; DB 4; Length 248;  
Query Match  
Best Local Similarity 43.4%; Pred. No. 2.2e-30;  
RESULT 1233  
ID AAU74770 standard; protein; 248 AA.  
DE Protein sequence of prostate homologue #2.  
PN WO200200708-A2.  
PD 03-JAN-2002.  
PA (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.  
Query Match  
Best Local Similarity 43.4%; Pred. No. 2.2e-30;  
RESULT 1234  
ID AAU74931 standard; protein; 248 AA.  
DE Amino acid sequence of prostate protein fragment #2.  
PN WO200200867-A1.  
PD 03-JAN-2002.  
PA (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.  
Query Match  
Best Local Similarity 43.4%; Pred. No. 2.2e-30;  
RESULT 1235  
ID AEG76997 standard; protein; 262 AA.  
DE Human kallikrein protein variant #1.  
PN WO200261131-A2.  
PD 08-AUG-2002.  
PA (BRIM) BRISTOL-MYERS SQUIBB CO.  
PA (TSUC/) TSUCHIHASHI Z.  
PA (HUIL/) HUI L. 36.0%; Score 495; DB 5; Length 262;  
Query Match  
Best Local Similarity 40.4%; Pred. No. 3e-30;  
RESULT 1236  
ID ADR90673 standard; protein; 246 AA.  
DE Human trypsinogen partial protein.  
PN WO2004078777-A2.  
PD 16-SEP-2004.  
PA (BIOR-) BIOREXIS PHARM CORP. 36.0%; Score 494.5; DB 8; Length 246;  
Query Match  
Best Local Similarity 41.9%; Pred. No. 3.1e-30;  
RESULT 1237  
ID AAB21321 standard; protein; 247 AA.  
DE Human trypsinogen.  
PN WO200053776-A2.  
PD 14-SEP-2000.  
PA (MOUN) MOUNT SINAI HOSPITAL.  
Query Match  
Best Local Similarity 41.9%; Pred. No. 3.1e-30;  
RESULT 1238  
ID ABR54239 standard; protein; 247 AA.  
DE Human NOV35a protein SEQ ID NO:146.  
PN WO2003023001-A2.  
PD 20-MAR-2003.  
PA (CURA-) CURAGEN CORP. 36.0%; Score 494.5; DB 6; Length 247;  
Query Match  
Best Local Similarity 41.9%; Pred. No. 3.1e-30;  
RESULT 1239  
ID ABR54241 standard; protein; 247 AA.  
DE Human NOV35c protein SEQ ID NO:150.  
PN WO2003023001-A2.  
PD 20-MAR-2003.  
PA (CURA-) CURAGEN CORP. 36.0%; Score 494.5; DB 6; Length 247;  
Query Match  
Best Local Similarity 41.9%; Pred. No. 3.1e-30;  
RESULT 1240  
ID ADQ30588 standard; protein; 247 AA.  
DE Pancreas cancer marker - trypsin I precursor.  
PN WO2004055519-A2.  
PD 01-JUL-2004.  
PA (HOFF) HOFFMANN LA ROCHE & CO AG F.  
PA (SINO-) SINOGENOMAX CO LTD CHINESE NAT HUMAN GEN. 36.0%; Score 494.5; DB 8; Length 247;  
Query Match  
Best Local Similarity 41.9%; Pred. No. 3.1e-30;  
RESULT 1241  
ID AAM01173 standard; protein; 254 AA.

DE Human prostate-specific amino acid mature form of P703P.  
PN WO200151633-A2.  
PD 19-JUL-2001.  
PA (CORI-) CORIXA CORP.  
Query Match 36.0%; Score 494; DB 4; Length 254;  
Best Local Similarity 42.7%; Pred. No. 3.5e-30;  
RESULT 1242  
ID AAU69818 standard; protein; 254 AA.  
DE Human prostate cDNA encoded protein #26.  
PN WO200173032-A2.  
PD 04-OCT-2001.  
PA (CORI-) CORIXA CORP.  
Query Match 36.0%; Score 494; DB 4; Length 254;  
Best Local Similarity 42.7%; Pred. No. 3.5e-30;  
RESULT 1243  
ID AAG99058 standard; protein; 254 AA.  
DE Human prostate-specific mature protein of P703P.  
PN WO200134802-A2.  
PD 17-MAY-2001.  
PA (CORI-) CORIXA CORP.  
Query Match 36.0%; Score 494; DB 4; Length 254;  
Best Local Similarity 42.7%; Pred. No. 3.5e-30;  
RESULT 1244  
ID ABU71709 standard; protein; 254 AA.  
DE Prostate cancer associated protein #12.  
PN US2002192763-A1.  
PD 19-DEC-2002.  
PA (XUJ/) XU J.  
PA (DILL/) DILLON D C.  
PA (MITC/) MITCHAM J L.  
PA (HARL/) HARLOCKER S L.  
PA (JIAN/) JIANG Y.  
PA (KALO/) KALOS M D.  
PA (FANG/) FANGER G R.  
PA (RETT/) RETTER M W.  
PA (STOL/) STOLK J A.  
PA (DAYC/) DAY C H.  
PA (VEDV/) VEDVICK T S.  
PA (CART/) CARTER D.  
PA (LISX/) LI S X.  
PA (WANG/) WANG A.  
PA (SKEI/) SKEIKY Y A W.  
PA (HEPL/) HEPLER W T.  
PA (HEND/) HENDERSON R A.  
PA (HURA/) HURAL J.  
PA (MCNE/) MCNEILL P D.  
PA (HOUG/) HOUGHTON R L.  
PA (DBAS/) Y DE BASSOLS C V.  
PA (FOYT/) FOY T M.  
Query Match 36.0%; Score 494; DB 4; Length 254;  
Best Local Similarity 42.7%; Pred. No. 3.5e-30;  
RESULT 1245  
ID ABB95278 standard; protein; 254 AA.  
DE Human P703P mature protein SEQ ID NO 523.  
PN US2002022248-A1.  
PD 21-FEB-2002.  
PA (XUJ/) XU J.  
PA (DILL/) DILLON D C.  
PA (MITC/) MITCHAM J L.  
PA (HARL/) HARLOCKER S L.  
PA (JIAN/) JIANG Y.  
PA (KALO/) KALOS M D.  
PA (FANG/) FANGER G R.  
PA (RETT/) RETTER M W.  
PA (STOL/) STOLK J A.  
PA (DAYC/) DAY C H.  
PA (VEDV/) VEDVICK T S.  
PA (CART/) CARTER D.  
PA (LISX/) LI S X.  
PA (WANG/) WANG A.  
PA (SKEI/) SKEIKY Y A W.  
PA (HEPL/) HEPLER W T.  
PA (HEND/) HENDERSON R A.

Query Match 36.0%; Score 494; DB 5; Length 254;  
Best Local Similarity 42.7%; Pred. No. 3.5e-30;  
RESULT 1246  
ID ABE54390 standard; protein; 254 AA.  
DE Prostate tumour specific protein sequence SEQ ID 523.  
PN WO200289747-A2.  
PD 14-NOV-2002.  
PA (CORI-) CORIXA CORP.  
Query Match 36.0%; Score 494; DB 6; Length 254;  
Best Local Similarity 42.7%; Pred. No. 3.5e-30;  
RESULT 1247  
ID ADB13973 standard; protein; 254 AA.  
DE Human mature prostate specific protein P703P.  
PN US2003185830-A1.  
PD 02-OCT-2003.  
PA (CORI-) CORIXA CORP.  
Query Match 36.0%; Score 494; DB 7; Length 254;  
Best Local Similarity 42.7%; Pred. No. 3.5e-30;  
RESULT 1248  
ID AG26389 standard; protein; 254 AA.  
DE Human prostate-specific polypeptide #59.  
PN US2003157089-A1.  
PD 21-AUG-2003.  
PA (CORI-) CORIXA CORP.  
Query Match 36.0%; Score 494; DB 7; Length 254;  
Best Local Similarity 42.7%; Pred. No. 3.5e-30;  
RESULT 1249  
ID AAB21319 standard; protein; 262 AA.  
DE Human KIX2.  
PN WO200053776-A2.  
PD 14-SEP-2000.  
PA (MOUN/) MOUNT SINAI HOSPITAL.  
Query Match 36.0%; Score 494; DB 3; Length 262;  
Best Local Similarity 40.4%; Pred. No. 3.6e-30;  
RESULT 1250  
ID ABG76996 standard; protein; 262 AA.  
DE Human kallikrein protein.  
PN WO200261131-A2.  
PD 08-AUG-2002.  
PA (BRIM/) BRISTOL-MYERS SQUIBB CO.  
PA (TSUC/) TSUCHIHASHI Z.  
PA (HUIL/) HUI L.  
Query Match 36.0%; Score 494; DB 5; Length 262;  
Best Local Similarity 40.4%; Pred. No. 3.6e-30;  
RESULT 1251  
ID ADL15197 standard; protein; 262 AA.  
DE Human pancreatic kallikrein.  
PN CN1384199-A.  
PD 11-DEC-2002.  
PA (REMI-) REMIN HOSPITAL SHENZHEN CITY.  
Query Match 36.0%; Score 494; DB 7; Length 262;  
Best Local Similarity 40.4%; Pred. No. 3.6e-30;  
RESULT 1252  
ID ADL64969 standard; protein; 262 AA.  
DE Human kallikrein protein (KLK1).  
PN US2004033582-A1.  
PD 19-FEB-2004.  
PA (EDMO/) EDMONDS M.  
PA (HUIL/) HUI L.  
PA (FERR/) FERRONE M.  
PA (POWE/) POWELL J R.  
PA (RAMA/) RAMANATHAN C S.  
PA (SWAN/) SWANSON B.  
PA (TSUC/) TSUCHIHASHI Z.  
PA (ZERB/) ZERBA K.  
Query Match 36.0%; Score 494; DB 8; Length 262;  
Best Local Similarity 40.4%; Pred. No. 3.6e-30;  
RESULT 1253  
ID ADQ39654 standard; protein; 262 AA.  
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1317.  
PN WO2004058052-A2.  
PD 15-JUL-2004.  
PA (APPL-) APPLERA CORP.

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Query Match 36.0%; Score 494; DB 8; Length 262;
Best Local Similarity 40.4%; Pred. No. 3.6e-30;
RESULT 1254
ID AD834891 standard; protein; 262 AA.
DE Human autoimmune disease-related protein - SEQ ID 105.
PN WO2004083403-A2.
PD 30-SEP-2004.
PA (APPL-) APPLERA CORP.
Query Match 36.0%; Score 494; DB 8; Length 262;
Best Local Similarity 40.4%; Pred. No. 3.6e-30;
RESULT 1255
ID ABR54277 standard; protein; 240 AA.
DE Human trypsinogen protein SEQ ID NO:341.
PN WO2003023001-A2.
PD 20-MAR-2003.
PA (CURA-) CURAGEN CORP.
Query Match 35.9%; Score 493.5; DB 6; Length 240;
Best Local Similarity 42.6%; Pred. No. 3.6e-30;
RESULT 1256
ID AAB21316 standard; protein; 241 AA.
DE Human trypsinogen.
PN WO2000053776-A2.
PD 14-SEP-2000.
PA (MOUN) MOUNT SINAI HOSPITAL.
Query Match 35.9%; Score 493.5; DB 3; Length 241;
Best Local Similarity 42.6%; Pred. No. 3.6e-30;
RESULT 1257
ID ADN04297 standard; protein; 247 AA.
DE Antiporatic protein sequence #343.
PN WO2004028479-A2.
PD 08-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 35.9%; Score 493; DB 8; Length 247;
Best Local Similarity 42.1%; Pred. No. 4.1e-30;
RESULT 1258
ID AAB21308 standard; protein; 253 AA.
DE Human EMSP.
PN WO2000053776-A2.
PD 14-SEP-2000.
PA (MOUN) MOUNT SINAI HOSPITAL.
Query Match 35.9%; Score 493; DB 3; Length 253;
Best Local Similarity 42.8%; Pred. No. 4.2e-30;
RESULT 1259
ID AAB21324 standard; protein; 258 AA.
DE Human EMSP.
PN WO2000053776-A2.
PD 14-SEP-2000.
PA (MOUN) MOUNT SINAI HOSPITAL.
Query Match 35.9%; Score 493; DB 3; Length 258;
Best Local Similarity 42.8%; Pred. No. 4.2e-30;
RESULT 1260
ID AAW71005 standard; protein; 262 AA.
DE Human prostate-associated kallikrein designated HPAK.
PN WO9833865-A1.
PD 30-JUL-1998.
PA (INCY-) INCYTE PHARM INC.
Query Match 35.9%; Score 493; DB 2; Length 262;
Best Local Similarity 40.4%; Pred. No. 4.3e-30;
RESULT 1261
ID ABP74711 standard; protein; 262 AA.
DE Human glandular kallikrein 1 precursor protein SEQ ID NO:600.
PN WO200281646-A2.
PD 17-OCT-2002.
PA (CTLI-) CTL IMMUNOTHERAPIES CORP.
Query Match 35.9%; Score 493; DB 6; Length 262;
Best Local Similarity 40.4%; Pred. No. 4.3e-30;
RESULT 1262
ID ADL15204 standard; protein; 262 AA.
DE Pancreatic kallikrein #1.
PN CN1384199-A.
PD 11-DEC-2002.
PA (REMI-) REMIN HOSPITAL SHENZHEN CITY.
Query Match 35.9%; Score 493; DB 7; Length 262;
Best Local Similarity 40.4%; Pred. No. 4.3e-30;
RESULT 1263
ID ADW72846 standard; protein; 263 AA.
DE Human glandular kallikrein 1 protein SEQ ID NO:105.
PN WO2004022709-A2.
PD 18-MAR-2004.
PA (MANN-) MANNKIND CORP.
Query Match 35.9%; Score 493; DB 8; Length 263;
Best Local Similarity 40.4%; Pred. No. 4.3e-30;
RESULT 1264
ID AAB98503 standard; protein; 225 AA.
DE Human trypsin serine protease catalytic domain.
PN WO200129056-A1.
PD 26-APR-2001.
PA (UYAR-) UNIV ARKANSAS.
Query Match 35.8%; Score 492; DB 4; Length 225;
Best Local Similarity 43.7%; Pred. No. 4.4e-30;
RESULT 1265
ID AAW93488 standard; protein; 230 AA.
DE Human TRYI trypsinogen variant protein.
PN WO9910503-A1.
PD 04-MAR-1999.
PA (HOFF) ROCHE DIAGNOSTICS GMBH.
Query Match 35.8%; Score 492; DB 2; Length 230;
Best Local Similarity 43.7%; Pred. No. 4.5e-30;
RESULT 1266
ID AAB21315 standard; protein; 256 AA.
DE Human KLK1.
PN WO2000053776-A2.
PD 14-SEP-2000.
PA (MOUN) MOUNT SINAI HOSPITAL.
Query Match 35.8%; Score 492; DB 3; Length 256;
Best Local Similarity 41.1%; Pred. No. 5e-30;
RESULT 1267
ID AAP95121 standard; protein; 262 AA.
DE Kallikrein encoded by clone lambda HK65a.
PN EP297913-A.
PD 04-JAN-1989.
PA (AMGE-) AMGEN.
Query Match 35.8%; Score 492; DB 1; Length 262;
Best Local Similarity 40.4%; Pred. No. 5.2e-30;
RESULT 1268
ID ABG76998 standard; protein; 262 AA.
DE Human kallikrein protein variant #2.
PN WO200261131-A2.
PD 08-AUG-2002.
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
PA (TSUC) TSUCHIHASHI Z.
PA (HUIL) HUI L.
Query Match 35.8%; Score 492; DB 5; Length 262;
Best Local Similarity 40.4%; Pred. No. 5.2e-30;
RESULT 1269
ID AAB54293 standard; protein; 267 AA.
DE Human pancreatic cancer antigen protein sequence SEQ ID NO:745.
PN WO200005320-A1.
PD 21-SEP-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 35.8%; Score 492; DB 3; Length 267;
Best Local Similarity 40.4%; Pred. No. 5.3e-30;
RESULT 1270
ID ABG77002 standard; protein; 262 AA.
DE Human kallikrein 1 polymorphic sequence.
PN WO200261131-A2.
PD 08-AUG-2002.
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
PA (TSUC) TSUCHIHASHI Z.
PA (HUIL) HUI L.
Query Match 35.7%; Score 491; DB 5; Length 262;
Best Local Similarity 40.4%; Pred. No. 6.2e-30;
RESULT 1271
ID ADA05744 standard; protein; 224 AA.
DE Human NOV18g protein SEQ ID NO:104.
PN WO2003029424-A2.
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PD 10-APR-2003.  
 PA (CURA-) CURAGEN CORP. 35.7%; Score 490; DB 6; Length 224;  
 Query Match 45.3%; Pred. No. 6.3e-30;  
 RESULT 1272  
 ID ADN62908 standard; protein; 224 AA.  
 DE Human NOV189.  
 PN US2004038223-A1.  
 PD 26-FEB-2004.  
 PA (SMIT/) SMITHSON G.  
 PA (MILL/) MILLET I.  
 PA (PEYM/) PEYMAN J A.  
 PA (KEKU/) KEKUDA R.  
 PA (JUUJ/) JU J.  
 PA (LILL/) LI L.  
 PA (GUOX/) GUO X.  
 PA (PATT/) PATTURAJAN M.  
 PA (SPYT/) SPYTEK K A.  
 PA (EDIN/) EDINGER S R.  
 PA (ELLE/) ELLERMAN K.  
 PA (MALY/) MALYANKAR U M.  
 PA (ORTT/) ORT T.  
 PA (GORM/) GORMAN L.  
 PA (ZERH/) ZERHUSEN B D.  
 PA (ANDE/) ANDERSON D W.  
 PA (ZHON/) ZHONG M.  
 PA (CATT/) CATTERTON E.  
 PA (JIWV/) JI W.  
 PA (MILL/) MILLER C E.  
 PA (RAST/) RASTELLI L.  
 PA (STON/) STONE D J.  
 PA (PENA/) PENA C E A.  
 PA (SHEN/) SHENOY S G.  
 PA (SHIM/) SHIMKETS R A.  
 PA (ROTH/) ROTHENBERG M E.  
 PA (LEAC/) LEACH M D.  
 PA (AGEE/) AGEE M L.  
 PA (BERG/) BERGHS C.  
 PA (DIPI/) DIPIPO V A.  
 PA (RISE/) EISEN A.  
 PA (GANG/) GANGOLLI E A.  
 PA (RIEG/) RIEGER D K.  
 PA (SPAD/) SPADERNA S K.  
 Query Match 35.7%; Score 490; DB 8; Length 224;  
 Best Local Similarity 45.3%; Pred. No. 6.3e-30;  
 RESULT 1273  
 ID AAE00397 standard; protein; 234 AA.  
 DE Human serine protease, PROST 07.  
 PN WO200125446-A1.  
 PD 12-APR-2001.  
 PA (SCHD ) SCHERING AG. 35.6%; Score 489.5; DB 4; Length 234;  
 Query Match 43.0%; Pred. No. 7.2e-30;  
 RESULT 1274  
 ID AAY25510 standard; protein; 231 AA.  
 DE Human prostate serine protease protein.  
 PN EP936370-A2.  
 PD 18-AUG-1999.  
 PA (BADI ) BASF AG. 35.6%; Score 488.5; DB 2; Length 231;  
 Query Match 43.9%; Pred. No. 8.4e-30;  
 RESULT 1275  
 ID ADN04726 standard; protein; 247 AA.  
 DE Antipsoriatic protein sequence #544.  
 PN WO2004028479-A2.  
 PD 08-APR-2004.  
 PA (GETH ) GENENTECH INC. 35.5%; Score 488; DB 8; Length 247;  
 Query Match 42.3%; Pred. No. 9.9e-30;  
 RESULT 1276  
 ID ADN99593 standard; protein; 247 AA.  
 DE Novel human protein sequence #409.  
 PN WO2004038003-A2.  
 Query Match 44.1%; Pred. No. 2e-29;  
 Best Local Similarity 44.1%; Pred. No. 2e-29;  
 PD 06-MAY-2004.  
 PA (FIVE-) FIVE PRIME THERAPEUTICS INC. 35.5%; Score 488; DB 8; Length 247;  
 Query Match 42.3%; Pred. No. 9.9e-30;  
 RESULT 1277  
 ID AM01227 standard; protein; 449 AA.  
 DE P703P and PSA fusion amino acid sequence.  
 PN WO200151633-A2.  
 PD 19-JUL-2001.  
 PA (CORI-) CORIXA CORP. 35.5%; Score 487.5; DB 4; Length 449;  
 Query Match 44.1%; Pred. No. 2e-29;  
 Best Local Similarity 44.1%; Pred. No. 2e-29;  
 RESULT 1278  
 ID AAU69872 standard; protein; 449 AA.  
 DE Human prostate serum antigen/P703P fusion protein.  
 PN WO200173032-A2.  
 PD 04-OCT-2001.  
 PA (CORI-) CORIXA CORP. 35.5%; Score 487.5; DB 4; Length 449;  
 Query Match 44.1%; Pred. No. 2e-29;  
 Best Local Similarity 44.1%; Pred. No. 2e-29;  
 RESULT 1279  
 ID ABU71763 standard; protein; 449 AA.  
 DE Prostate cancer specific antigen fusion protein #1.  
 PN US2002192763-A1.  
 PD 19-DEC-2002.  
 PA (XUJJ/) XU J.  
 PA (DILL/) DILLON D C.  
 PA (MITC/) MITCHAM J L.  
 PA (HARL/) HARLOCKER S L.  
 PA (JIAN/) JIANG Y.  
 PA (KALO/) KALOS M D.  
 PA (FANG/) FANGER G R.  
 PA (RETT/) RETTER M W.  
 PA (STOL/) STOLK J A.  
 PA (DAYC/) DAY C H.  
 PA (VEDV/) VEDVICK T S.  
 PA (CART/) CARTER D.  
 PA (LISX/) LI S X.  
 PA (WANG/) WANG A.  
 PA (SKEI/) SKEIKY Y A W.  
 PA (HEPL/) HEPLER W T.  
 PA (HEND/) HENDERSON R A.  
 PA (HURA/) HURAL J.  
 PA (MCNE/) MCNEILL P D.  
 PA (HOUG/) HOUGHTON R L.  
 PA (DBAS/) Y DE BASSOLS C V.  
 PA (FOYT/) FOY T M. 35.5%; Score 487.5; DB 4; Length 449;  
 Query Match 44.1%; Pred. No. 2e-29;  
 Best Local Similarity 44.1%; Pred. No. 2e-29;  
 RESULT 1280  
 ID ABB95332 standard; protein; 449 AA.  
 DE Human P703P/PSA fusion protein SEQ ID NO 617.  
 PN US2002022248-A1.  
 PD 21-FEB-2002.  
 PA (XUJJ/) XU J.  
 PA (DILL/) DILLON D C.  
 PA (MITC/) MITCHAM J L.  
 PA (HARL/) HARLOCKER S L.  
 PA (JIAN/) JIANG Y.  
 PA (KALO/) KALOS M D.  
 PA (FANG/) FANGER G R.  
 PA (RETT/) RETTER M W.  
 PA (STOL/) STOLK J A.  
 PA (DAYC/) DAY C H.  
 PA (VEDV/) VEDVICK T S.  
 PA (CART/) CARTER D.  
 PA (LISX/) LI S X.  
 PA (WANG/) WANG A.  
 PA (SKEI/) SKEIKY Y A W.  
 PA (HEPL/) HEPLER W T.  
 PA (HEND/) HENDERSON R A. 35.5%; Score 487.5; DB 5; Length 449;  
 Query Match 44.1%; Pred. No. 2e-29;  
 Best Local Similarity 44.1%; Pred. No. 2e-29;

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RESULT 1281
ID ABR54444 standard; protein; 449 AA.
DE Prostate tumour specific protein sequence SEQ ID 617.
PN WO200289747-A2.
PD 14-NOV-2002.
PA (CORI-) CORIXA CORP. 35.5%; Score 487.5; DB 6; Length 449;
Query Match
Best Local Similarity 44.1%; Pred. No. 2e-29;
RESULT 1282
ID ADB14067 standard; protein; 449 AA.
DE Human prostate specific protein P703P/PSA fusion protein.
PN US2003185830-A1.
PD 02-OCT-2003.
PA (CORI-) CORIXA CORP. 35.5%; Score 487.5; DB 7; Length 449;
Query Match
Best Local Similarity 44.1%; Pred. No. 2e-29;
RESULT 1283
ID ADG26483 standard; protein; 449 AA.
DE Human prostate-specific polypeptide #113.
PN US2003157089-A1.
PD 21-AUG-2003.
PA (CORI-) CORIXA CORP. 35.5%; Score 487.5; DB 7; Length 449;
Query Match
Best Local Similarity 44.1%; Pred. No. 2e-29;
RESULT 1284
ID ABU71889 standard; protein; 585 AA.
DE Prostate cancer specific antigen fusion protein #3.
PN US2002192763-A1.
PD 19-DEC-2002.
PA (XUJJ/) XU J.
PA (DILL/) DILLON D C.
PA (MITC/) MITCHAM J L.
PA (HARL/) HARLOCKER S L.
PA (JIAN/) JIANG Y.
PA (KALO/) KALOS M D.
PA (FANG/) FANGER G R.
PA (RETT/) RETTER M W.
PA (STOL/) STOLK J A.
PA (DAYC/) DAY C H.
PA (VEDV/) VEDVICK T S.
PA (CART/) CARTER D.
PA (LISX/) LI S X.
PA (WANG/) WANG A.
PA (SKEI/) SKEIKY Y A W.
PA (HEPL/) HEPLER W T.
PA (HEND/) HENDERSON R A.
PA (HURA/) HURAL J.
PA (MCNE/) MCNEILL P D.
PA (HOUG/) HOUGHTON R L.
PA (DBAS/) Y DE BASSOLS C V.
PA (FOYT/) FOY T M.
Query Match
Best Local Similarity 44.1%; Pred. No. 2.6e-29;
RESULT 1285
ID ABU71888 standard; protein; 585 AA.
DE Prostate cancer associated protein #72.
PN US2002192763-A1.
PD 19-DEC-2002.
PA (XUJJ/) XU J.
PA (DILL/) DILLON D C.
PA (MITC/) MITCHAM J L.
PA (HARL/) HARLOCKER S L.
PA (JIAN/) JIANG Y.
PA (KALO/) KALOS M D.
PA (FANG/) FANGER G R.
PA (RETT/) RETTER M W.
PA (STOL/) STOLK J A.
PA (DAYC/) DAY C H.
PA (VEDV/) VEDVICK T S.
PA (CART/) CARTER D.
PA (LISX/) LI S X.
PA (WANG/) WANG A.
PA (SKEI/) SKEIKY Y A W.
Query Match
Best Local Similarity 44.1%; Pred. No. 2.6e-29;
RESULT 1286
ID ABR54580 standard; protein; 585 AA.
DE Prostate tumour-related protein SEQ ID 1020.
PN WO200289747-A2.
PD 14-NOV-2002.
PA (FOYT/) FOY T M.
Query Match
Best Local Similarity 44.1%; Pred. No. 2.6e-29;
RESULT 1287
ID ADB14470 standard; protein; 585 AA.
DE FOPP/hpAP fusion protein, FOPP3.
PN US2003185830-A1.
PD 02-OCT-2003.
PA (CORI-) CORIXA CORP. 35.5%; Score 487.5; DB 7; Length 585;
Query Match
Best Local Similarity 44.1%; Pred. No. 2.6e-29;
RESULT 1288
ID AG26993 standard; protein; 585 AA.
DE Human prostate-specific polypeptide #249.
PN US2003157089-A1.
PD 21-AUG-2003.
PA (CORI-) CORIXA CORP. 35.5%; Score 487.5; DB 7; Length 585;
Query Match
Best Local Similarity 44.1%; Pred. No. 2.6e-29;
RESULT 1289
ID AEU71890 standard; protein; 801 AA.
DE Prostate cancer specific antigen fusion protein #4.
PN US2002192763-A1.
PD 19-DEC-2002.
PA (XUJJ/) XU J.
PA (DILL/) DILLON D C.
PA (MITC/) MITCHAM J L.
PA (HARL/) HARLOCKER S L.
PA (JIAN/) JIANG Y.
PA (KALO/) KALOS M D.
PA (FANG/) FANGER G R.
PA (RETT/) RETTER M W.
PA (STOL/) STOLK J A.
PA (DAYC/) DAY C H.
PA (VEDV/) VEDVICK T S.
PA (CART/) CARTER D.
PA (LISX/) LI S X.
PA (WANG/) WANG A.
PA (SKEI/) SKEIKY Y A W.
PA (HEPL/) HEPLER W T.
PA (HEND/) HENDERSON R A.
PA (HURA/) HURAL J.
PA (MCNE/) MCNEILL P D.
PA (HOUG/) HOUGHTON R L.
PA (DBAS/) Y DE BASSOLS C V.
PA (FOYT/) FOY T M.
Query Match
Best Local Similarity 44.1%; Pred. No. 3.6e-29;
RESULT 1290
ID RAY31160 standard; protein; 224 AA.
DE Human trypsin serine protease protein domain.
PN US5948892-A.
PD 07-SEP-1999.
PA (AMGE-) AMGEN INC.
Query Match
Best Local Similarity 43.4%; Pred. No. 1.1e-29;
RESULT 1291
ID ADL15207 standard; protein; 261 AA.
DE Pancreatic kallikrein #3.
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PN CN1384199-A.  
PD 11-DEC-2002.  
PA (REMI-) REMIN HOSPITAL SHENZHEN CITY.  
Query Match 35.3%; Score 484.5; DB 7; Length 261;  
Best Local Similarity 40.2%; Pred. No. 1.9e-29;  
RESULT 1292  
ID AAM83249 standard; protein; 261 AA.  
DE Human diagnostic and therapeutic pproteins SEQ ID NO:3498.  
PN WO2004023973-A2.  
PD 25-MAR-2004.  
PA (INCY-) INCYTE CORP.  
Query Match 35.2%; Score 484; DB 8; Length 261;  
Best Local Similarity 43.5%; Pred. No. 2.1e-29;  
RESULT 1293  
ID AAM83250 standard; protein; 333 AA.  
DE Human diagnostic and therapeutic pproteins SEQ ID NO:3499.  
PN WO2004023973-A2.  
PD 25-MAR-2004.  
PA (INCY-) INCYTE CORP.  
Query Match 35.2%; Score 484; DB 8; Length 333;  
Best Local Similarity 43.5%; Pred. No. 2.7e-29;  
RESULT 1294  
ID AAW57740 standard; protein; 240 AA.  
DE Trypsinogen-like protein.  
PN JP1009080-A.  
PD 21-APR-1998.  
PA (SHIS-) SHISEIDO CO LTD.  
Query Match 35.2%; Score 483.5; DB 2; Length 240;  
Best Local Similarity 42.5%; Pred. No. 2.1e-29;  
RESULT 1295  
ID ADL15206 standard; protein; 260 AA.  
DE Pancreatic kallikrein #2.  
PN CN1384199-A.  
PD 11-DEC-2002.  
PA (REMI-) REMIN HOSPITAL SHENZHEN CITY.  
Query Match 35.2%; Score 483; DB 7; Length 260;  
Best Local Similarity 39.8%; Pred. No. 2.5e-29;  
RESULT 1296  
ID AAB21293 standard; protein; 237 AA.  
DE Human KLK-L1 protein #1.  
PN WO200053776-A2.  
PD 14-SEP-2000.  
PA (MOUN-) MOUNT SINAI HOSPITAL.  
Query Match 35.1%; Score 482.5; DB 3; Length 237;  
Best Local Similarity 42.2%; Pred. No. 2.5e-29;  
RESULT 1297  
ID AAP70568 standard; protein; 262 AA.  
DE Human kallikrein-like substance has hypotensive activity.  
PN JP62126980-A.  
PD 09-JUN-1987.  
PA (NAKA-) NAKANISHI S.  
Query Match 35.0%; Score 481; DB 1; Length 262;  
Best Local Similarity 40.0%; Pred. No. 3.6e-29;  
RESULT 1298  
ID AAU01290 standard; protein; 216 AA.  
DE Human serine protease HETAA37p.  
PN WO200123587-A2.  
PD 05-APR-2001.  
PA (SMIK-) SMITHKLINE BEECHAM PLC.  
Query Match 34.8%; Score 477.5; DB 4; Length 216;  
Best Local Similarity 44.3%; Pred. No. 5.5e-29;  
RESULT 1299  
ID AAY72526 standard; protein; 226 AA.  
DE Human prostatic antigen P703PDE5 sequence.  
PN WO200104143-A2.  
PD 18-JAN-2001.  
PA (SMIK-) SMITHKLINE BEECHAM BIOLOGICALS.  
PA (CORI-) CORIAX CORP.  
Query Match 34.8%; Score 477.5; DB 4; Length 226;  
Best Local Similarity 43.8%; Pred. No. 5.8e-29;  
RESULT 1300  
ID AAU74902 standard; protein; 226 AA.  
DE Protein sequence of prostate homologue #4.  
PN WO200200708-A2.  
PD 03-JAN-2002.  
PA (SMIK-) SMITHKLINE BEECHAM BIOLOGICALS.  
Query Match 34.8%; Score 477.5; DB 5; Length 226;  
Best Local Similarity 43.8%; Pred. No. 5.8e-29;  
RESULT 1301  
ID AAU74933 standard; protein; 226 AA.  
DE Amino acid sequence of prostate protein fragment #4.  
PN WO200200867-A1.  
PD 03-JAN-2002.  
PA (SMIK-) SMITHKLINE BEECHAM BIOLOGICALS.  
Query Match 34.8%; Score 477.5; DB 5; Length 226;  
Best Local Similarity 43.8%; Pred. No. 5.8e-29;  
RESULT 1302  
ID AAY72522 standard; protein; 312 AA.  
DE NSI-P703P-His fusion protein.  
PN WO200104143-A2.  
PD 18-JAN-2001.  
PA (SMIK-) SMITHKLINE BEECHAM BIOLOGICALS.  
PA (CORI-) CORIAX CORP.  
Query Match 34.8%; Score 477.5; DB 4; Length 312;  
Best Local Similarity 43.8%; Pred. No. 8.1e-29;  
RESULT 1303  
ID AAU74768 standard; protein; 312 AA.  
DE Amino acid sequence of wild-type NSI-p703-His fusion protein.  
PN WO200200708-A2.  
PD 03-JAN-2002.  
PA (SMIK-) SMITHKLINE BEECHAM BIOLOGICALS.  
Query Match 34.8%; Score 477.5; DB 5; Length 312;  
Best Local Similarity 43.8%; Pred. No. 8.1e-29;  
RESULT 1304  
ID AAU74929 standard; protein; 312 AA.  
DE Amino acid sequence of wild-type NSI-P703P-His fusion protein.  
PN WO200200867-A1.  
PD 03-JAN-2002.  
PA (SMIK-) SMITHKLINE BEECHAM BIOLOGICALS.  
Query Match 34.8%; Score 477.5; DB 5; Length 312;  
Best Local Similarity 43.8%; Pred. No. 8.1e-29;  
RESULT 1305  
ID ABU71886 standard; protein; 344 AA.  
DE Human prostate specific antigen (PSA) epitope #26.  
PN US2002192763-A1.  
PD 19-DEC-2002.  
PA (XUJ-) XU J.  
PA (DILL-) DILLON D C.  
PA (MITC-) MITCHAM J L.  
PA (HARL-) HARLOCKER S L.  
PA (JIAN-) JIANG Y.  
PA (KALO-) KALOS M D.  
PA (FANG-) FANGER G R.  
PA (BETT-) BETTER M W.  
PA (STOL-) STOLK J A.  
PA (DAYC-) DAY C H.  
PA (VEDV-) VEDVICK T S.  
PA (CART-) CARTER D.  
PA (LISX-) LI S X.  
PA (WANG-) WANG A.  
PA (SKEI-) SKEIKY Y A W.  
PA (HEPL-) HEPLER W T.  
PA (HEND-) HENDERSON R A.  
PA (HURA-) HURAL J.  
PA (MCNE-) MCNEILL P D.  
PA (HOUG-) HOUGHTON R L.  
PA (DBAS-) Y DE BASSOLS C V.  
PA (FOYT-) FOY T M.  
Query Match 34.8%; Score 477.5; DB 4; Length 344;  
Best Local Similarity 43.8%; Pred. No. 8.9e-29;  
RESULT 1306  
ID AAM82601 standard; protein; 239 AA.  
DE Human diagnostic and therapeutic pproteins SEQ ID NO:2850.  
PN WO2004023973-A2.  
PD 25-MAR-2004.  
PA (INCY-) INCYTE CORP.

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Query Match
Best Local Similarity 34.6%; Score 475.5; DB 8; Length 239;
RESULT 1307
ID ABR1659 standard; protein; 220 AA.
DE Prostate cancer specific antigen P703P #4.
PN US2002192763-A1.
PD 19-DEC-2002.
PA (XUJ)/ XU J.
PA (DILL)/ DILLON D C.
PA (MITC)/ MITCHAM J L.
PA (HARL)/ HARLOCKER S L.
PA (JIAN)/ JIANG Y.
PA (KALO)/ KALOS M D.
PA (FANG)/ FANGER G R.
PA (RETT)/ RETTER M W.
PA (STOL)/ STOLK J A.
PA (DAYC)/ DAY C H.
PA (VEDV)/ VEDVICK T S.
PA (CART)/ CARTER D.
PA (LISX)/ LI S X.
PA (WANG)/ WANG A.
PA (SKEI)/ SKEIKY Y A W.
PA (HEPL)/ HEPLER W T.
PA (HEND)/ HENDERSON R A.
PA (HURA)/ HURAL J.
PA (MCNE)/ MCNEILL P D.
PA (HUG)/ HOUGHTON R L.
PA (DBAS)/ Y DE BASSOLS C V.
PA (FOYT)/ FOY T M.
Query Match
Best Local Similarity 34.4%; Score 472.5; DB 4; Length 220;
RESULT 1316
ID ABR5228 standard; protein; 220 AA.
DE Human P703PDE5 protein SEQ ID NO 327.
PN US2002022248-A1.
PD 21-FEB-2002.
PA (XUJ)/ XU J.
PA (DILL)/ DILLON D C.
PA (MITC)/ MITCHAM J L.
PA (HARL)/ HARLOCKER S L.
PA (JIAN)/ JIANG Y.
PA (KALO)/ KALOS M D.
PA (FANG)/ FANGER G R.
PA (RETT)/ RETTER M W.
PA (STOL)/ STOLK J A.
PA (DAYC)/ DAY C H.
PA (VEDV)/ VEDVICK T S.
PA (CART)/ CARTER D.
PA (LISX)/ LI S X.
PA (WANG)/ WANG A.
PA (SKEI)/ SKEIKY Y A W.
PA (HEPL)/ HEPLER W T.
PA (HEND)/ HENDERSON R A.
Query Match
Best Local Similarity 34.4%; Score 472.5; DB 5; Length 220;
RESULT 1318
ID ABR5430 standard; protein; 220 AA.
DE Prostate tumour specific protein sequence SEQ ID 327.
PN WO200289747-A2.
PD 14-NOV-2002.
PA (CORI-) CORIXA CORP.
Query Match
Best Local Similarity 34.4%; Score 472.5; DB 6; Length 220;
RESULT 1319
ID ADB13777 standard; protein; 220 AA.
DE Human prostate specific protein P703PDE5.
PN US2003185830-A1.
PD 02-OCT-2003.
PA (CORI-) CORIXA CORP.
Query Match
Best Local Similarity 34.4%; Score 472.5; DB 7; Length 220;
RESULT 1320
ID ADG26193 standard; protein; 220 AA.
DE Human prostate-specific polypeptide #9.
Query Match
Best Local Similarity 34.6%; Score 475.5; DB 8; Length 239;
RESULT 1307
ID ABR1659 standard; protein; 220 AA.
DE Human diagnostic and therapeutic pprotein SEQ ID NO:2851.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match
Best Local Similarity 34.6%; Score 475.5; DB 8; Length 239;
RESULT 1308
ID ABR2603 standard; protein; 239 AA.
DE Human diagnostic and therapeutic pprotein SEQ ID NO:2852.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match
Best Local Similarity 34.6%; Score 475.5; DB 8; Length 239;
RESULT 1309
ID ADN99649 standard; protein; 280 AA.
DE Novel human protein sequence #465.
PN WO2004038003-A2.
PD 06-MAY-2004.
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
Query Match
Best Local Similarity 34.4%; Score 473; DB 8; Length 280;
RESULT 1310
ID AAY82008 standard; protein; 220 AA.
DE Human immunogenic prostate tumour protein sequence SEQ ID NO:327.
PN WO200004149-A2.
PD 27-JAN-2000.
PA (CORI-) CORIXA CORP.
Query Match
Best Local Similarity 34.4%; Score 472.5; DB 3; Length 220;
RESULT 1311
ID AAM01123 standard; protein; 220 AA.
DE Human prostate-specific amino acid sequence P703PDE6.
PN WO200151633-A2.
PD 19-JUL-2001.
PA (CORI-) CORIXA CORP.
Query Match
Best Local Similarity 34.4%; Score 472.5; DB 4; Length 220;
RESULT 1312
ID AAU69768 standard; protein; 220 AA.
DE Human prostate cDNA encoded protein #8.
PN WO200173032-A2.
PD 04-OCT-2001.
PA (CORI-) CORIXA CORP.
Query Match
Best Local Similarity 34.4%; Score 472.5; DB 4; Length 220;
RESULT 1313
ID AAB74806 standard; protein; 220 AA.
DE Prostate tumour antigen predicted amino acid sequence for P703PDE5.
PN WO200125272-A2.
PD 12-APR-2001.
PA (CORI-) CORIXA CORP.
Query Match
Best Local Similarity 34.4%; Score 472.5; DB 4; Length 220;
RESULT 1314
ID AAG99008 standard; protein; 220 AA.
DE Human prostate-specific amino acid sequence P703PDE5.
PN WO200134802-A2.
PD 17-MAY-2001.
PA (CORI-) CORIXA CORP.
Query Match
Best Local Similarity 34.4%; Score 472.5; DB 4; Length 220;
RESULT 1315
ID AAG62147 standard; protein; 220 AA.
DE Human P703P inventive antigen SEQ ID NO: 330.
PN WO200125273-A2.
PD 12-APR-2001.
PA (CORI-) CORIXA CORP.
Query Match
Best Local Similarity 34.4%; Score 472.5; DB 4; Length 220;
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PN US2003157089-A1.  
PD 21-AUG-2003.  
PA (CORI-) CORIXA CORP.  
Query Match 34.4%; Score 472.5; DB 7; Length 220;  
Best Local Similarity 43.8%; Pred. No. 1.4e-28;  
RESULT 1321  
ID ADI39732 standard; protein; 262 AA.  
DE Human glandular kallikrein (HK2) protein.  
PN US6642013-B1.  
PD 04-NOV-2003.  
PA (UYAR-) UNIV ARKANSAS MEDICAL SCI.  
Query Match 34.4%; Score 472.5; DB 8; Length 262;  
Best Local Similarity 38.9%; Pred. No. 1.6e-28;  
RESULT 1322  
ID ADI37156 standard; protein; 262 AA.  
DE Human glandular kallikrein (hHK2) protein.  
PN US200319010-A1.  
PD 23-OCT-2003.  
PA (UYAR-) UNIV ARKANSAS.  
Query Match 34.4%; Score 472.5; DB 8; Length 262;  
Best Local Similarity 38.9%; Pred. No. 1.6e-28;  
RESULT 1323  
ID ABR96163 standard; protein; 274 AA.  
DE Human NOVI2a protein SEQ ID NO:68.  
PN WO200290568-A2.  
PD 14-NOV-2002.  
PA (CURA-) CURAGEN CORP.  
Query Match 34.4%; Score 472.5; DB 6; Length 274;  
Best Local Similarity 40.7%; Pred. No. 1.7e-28;  
RESULT 1324  
ID AAP92314 standard; protein; 245 AA.  
DE Human recombinant kallikrein gene.  
PN EP297913-A.  
PD 04-JAN-1989.  
PA (AMGE-) AMGEN.  
Query Match 34.3%; Score 471; DB 1; Length 245;  
Best Local Similarity 40.2%; Pred. No. 2e-28;  
RESULT 1325  
ID AAB21313 standard; protein; 255 AA.  
DE Human PSA.  
PN WO200053776-A2.  
PD 14-SEP-2000.  
PA (MOUN) MOUNT SINAI HOSPITAL.  
Query Match 34.2%; Score 470.5; DB 3; Length 255;  
Best Local Similarity 40.4%; Pred. No. 2.3e-28;  
RESULT 1326  
ID AAU06276 standard; protein; 257 AA.  
DE Prostate specific Antigen (PSA) polypeptide.  
PN WO200145728-A2.  
PD 28-JUN-2001.  
PA (EPIM-) EPIMUNE INC.  
Query Match 34.2%; Score 470.5; DB 4; Length 257;  
Best Local Similarity 40.4%; Pred. No. 2.3e-28;  
RESULT 1327  
ID AAW13649 standard; protein; 261 AA.  
DE Human prostatic specific antigen.  
PN WO9711172-A1.  
PD 27-MAR-1997.  
PA (WORC-) WORCESTER FOUND BIOMEDICAL RES.  
Query Match 34.2%; Score 470.5; DB 2; Length 261;  
Best Local Similarity 40.4%; Pred. No. 2.3e-28;  
RESULT 1328  
ID AAY56048 standard; protein; 261 AA.  
DE Human prostate-specific antigen.  
PN WO9961068-A1.  
PD 02-DEC-1999.  
PA (UYPE-) UNIV PENNSYLVANIA.  
Query Match 34.2%; Score 470.5; DB 3; Length 261;  
Best Local Similarity 40.4%; Pred. No. 2.3e-28;  
RESULT 1329  
ID AAY77842 standard; protein; 261 AA.  
DE Human prostate-specific antigen (PSA) sequence.  
PN WO9960984-A2.

PD 02-DEC-1999.  
PA (ENTR-) ENTREMED INC.  
Query Match 34.2%; Score 470.5; DB 3; Length 261;  
Best Local Similarity 40.4%; Pred. No. 2.3e-28;  
RESULT 1330  
ID AAB21317 standard; protein; 261 AA.  
DE Human PSA.  
PN WO200053776-A2.  
PD 14-SEP-2000.  
PA (MOUN) MOUNT SINAI HOSPITAL.  
Query Match 34.2%; Score 470.5; DB 3; Length 261;  
Best Local Similarity 40.4%; Pred. No. 2.3e-28;  
RESULT 1331  
ID AAB74821 standard; protein; 261 AA.  
DE Prostate tumour antigen amino acid sequence for PSA.  
PN WO200125272-A2.  
PD 12-APR-2001.  
PA (CORI-) CORIXA CORP.  
Query Match 34.2%; Score 470.5; DB 4; Length 261;  
Best Local Similarity 40.4%; Pred. No. 2.3e-28;  
RESULT 1332  
ID AAG62144 standard; protein; 261 AA.  
DE Human prostate specific membrane antigen SEQ ID NO: 327.  
PN WO200125273-A2.  
PD 12-APR-2001.  
PA (CORI-) CORIXA CORP.  
Query Match 34.2%; Score 470.5; DB 4; Length 261;  
Best Local Similarity 40.4%; Pred. No. 2.3e-28;  
RESULT 1333  
ID AAG62146 standard; protein; 261 AA.  
DE Human prostate specific antigen SEQ ID NO: 329.  
PN WO200125273-A2.  
PD 12-APR-2001.  
PA (CORI-) CORIXA CORP.  
Query Match 34.2%; Score 470.5; DB 4; Length 261;  
Best Local Similarity 40.4%; Pred. No. 2.3e-28;  
RESULT 1334  
ID ABU71859 standard; protein; 261 AA.  
DE Human prostatic specific membrane antigen (PSMA).  
PN US2002192763-A1.  
PD 19-DEC-2002.  
PA (XUJ) XU J.  
PA (DILL) DILLON D C.  
PA (MITC) MITCHAM J L.  
PA (HARL) HARLOCKER S L.  
PA (JIAN) JIANG Y.  
PA (KALO) KALOS M D.  
PA (FANG) FANGER G R.  
PA (RETT) RETTER M W.  
PA (STOL) STOLK J A.  
PA (DAYC) DAY C H.  
PA (VEDV) VEDVICK T S.  
PA (CART) CARTER D.  
PA (LISK) LI S X.  
PA (WANG) WANG A.  
PA (SKEI) SKEIKY Y A W.  
PA (HEPL) HEPLER W T.  
PA (HEND) HENDERSON R A.  
PA (HURA) HURAL J.  
PA (MCNE) MCNEILL P D.  
PA (HOUG) HOUGHTON R L.  
PA (DBAS) Y DE BASSOLS C V.  
PA (FOYT) FOY T M.  
Query Match 34.2%; Score 470.5; DB 4; Length 261;  
Best Local Similarity 40.4%; Pred. No. 2.3e-28;  
RESULT 1335  
ID ABF74202 standard; protein; 261 AA.  
DE Human PSA protein SEQ ID NO:78.  
PN WO200281646-A2.  
PD 17-OCT-2002.  
PA (CYLI-) CTL IMMUNOTHERAPIES CORP.  
Query Match 34.2%; Score 470.5; DB 6; Length 261;  
Best Local Similarity 40.4%; Pred. No. 2.3e-28;

RESULT 1336  
ID ADB82777 standard; protein; 261 AA.  
DE Human protein sequence useful for the treatment of cancer (SeqID 1558).  
PN WO2003050236-A2.  
PD 19-JUN-2003.  
PA (CHIR ) CHIRON CORP.  
PA (HYSE-) HYSEQ INC.  
Query Match 34.2%; Score 470.5; DB 7; Length 261;  
Best Local Similarity 40.4%; Pred. No. 2.3e-28;  
RESULT 1337  
ID ADC09580 standard; protein; 261 AA.  
DE PSA protein #SEQ ID 78.  
PN WO2003008537-A2.  
PD 30-JAN-2003.  
PA (CTL-) CTL IMMUNOTHERAPIES CORP.  
Query Match 34.2%; Score 470.5; DB 7; Length 261;  
Best Local Similarity 40.4%; Pred. No. 2.3e-28;  
RESULT 1338  
ID ADJ59022 standard; protein; 261 AA.  
DE Human PSA precursor protein sequence.  
PN WO2003047506-A2.  
PD 12-JUN-2003.  
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
Query Match 34.2%; Score 470.5; DB 7; Length 261;  
Best Local Similarity 40.4%; Pred. No. 2.3e-28;  
RESULT 1339  
ID ADI39733 standard; protein; 261 AA.  
DE Human prostate specific antigen (PSA) protein.  
PN US6642013-B1.  
PD 04-NOV-2003.  
PA (UYAR-) UNIV ARKANSAS MEDICAL SCI.  
Query Match 34.2%; Score 470.5; DB 8; Length 261;  
Best Local Similarity 40.4%; Pred. No. 2.3e-28;  
RESULT 1340  
ID ADI37157 standard; protein; 261 AA.  
DE Human prostate specific antigen (hPSA).  
PN US2003199010-A1.  
PD 23-OCT-2003.  
PA (UYAR-) UNIV ARKANSAS.  
Query Match 34.2%; Score 470.5; DB 8; Length 261;  
Best Local Similarity 40.4%; Pred. No. 2.3e-28;  
RESULT 1341  
ID ADM72819 standard; protein; 261 AA.  
DE Human PSA protein SEQ ID NO:78.  
PN WO2004022709-A2.  
PD 18-MAR-2004.  
PA (MANN-) MANNKIND CORP.  
Query Match 34.2%; Score 470.5; DB 8; Length 261;  
Best Local Similarity 40.4%; Pred. No. 2.3e-28;  
RESULT 1342  
ID ABM82166 standard; protein; 261 AA.  
DE Tumour-associated antigenic target (TAT) polypeptide PRO2109, SEQ:5591.  
PN WO2004030615-A2.  
PD 15-APR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 34.2%; Score 470.5; DB 8; Length 261;  
Best Local Similarity 40.4%; Pred. No. 2.3e-28;  
RESULT 1343  
ID AAB08449 standard; protein; 375 AA.  
DE A human prostate specific antigen variant polypeptide.  
PN WO200049158-A2.  
PD 24-AUG-2000.  
PA (COMP-) COMPUGEN LTD.  
Query Match 34.2%; Score 470.5; DB 3; Length 375;  
Best Local Similarity 40.4%; Pred. No. 3.4e-28;  
RESULT 1344  
ID AAG62154 standard; protein; 692 AA.  
DE Human WTI/PSA fusion protein SEQ ID NO: 357.  
PN WO200125273-A2.  
PD 12-APR-2001.  
PA (CORI-) CORIXA CORP.  
Query Match 34.2%; Score 470.5; DB 4; Length 692;  
Best Local Similarity 40.4%; Pred. No. 6.3e-28;

RESULT 1345  
ID AAB67545 standard; protein; 284 AA.  
DE Amino acid sequence of protease MH2 catalytic domain in PFEK2-6XHIS-TAG.  
PN WO200116289-A2.  
PD 08-MAR-2001.  
PA (ORTH ) ORTHO-MCNEIL PHARM INC.  
Query Match 34.1%; Score 469; DB 4; Length 284;  
Best Local Similarity 43.8%; Pred. No. 3.3e-28;  
RESULT 1346  
ID ADJ59024 standard; protein; 261 AA.  
DE Human PSA precursor protein sequence.  
PN WO2003047506-A2.  
PD 12-JUN-2003.  
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
Query Match 34.1%; Score 468.5; DB 7; Length 261;  
Best Local Similarity 40.4%; Pred. No. 3.3e-28;  
RESULT 1347  
ID AAU74903 standard; protein; 231 AA.  
DE Amino acid sequence of p703 mutated-His fusion protein.  
PN WO200200708-A2.  
PD 03-JAN-2002.  
PA (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.  
Query Match 34.0%; Score 467.5; DB 5; Length 231;  
Best Local Similarity 43.4%; Pred. No. 3.5e-28;  
RESULT 1348  
ID AAU74934 standard; protein; 231 AA.  
DE Amino acid sequence of P703P mutated-His fusion protein.  
PN WO200200867-A1.  
PD 03-JAN-2002.  
PA (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.  
Query Match 34.0%; Score 467.5; DB 5; Length 231;  
Best Local Similarity 43.4%; Pred. No. 3.5e-28;  
RESULT 1349  
ID AAY72521 standard; protein; 312 AA.  
DE NS1-P703P mutated-His fusion protein.  
PN WO200104143-A2.  
PD 18-JAN-2001.  
PA (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.  
PA (CORI-) CORIXA CORP.  
Query Match 34.0%; Score 467.5; DB 4; Length 312;  
Best Local Similarity 43.4%; Pred. No. 4.8e-28;  
RESULT 1350  
ID AAU74767 standard; protein; 312 AA.  
DE Amino acid sequence of NS1-p703 mutated-His fusion protein.  
PN WO200200708-A2.  
PD 03-JAN-2002.  
PA (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.  
Query Match 34.0%; Score 467.5; DB 5; Length 312;  
Best Local Similarity 43.4%; Pred. No. 4.8e-28;  
RESULT 1351  
ID AAU74928 standard; protein; 312 AA.  
DE Amino acid sequence of NS1-P703P mutated-His fusion protein.  
PN WO200200867-A1.  
PD 03-JAN-2002.  
PA (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.  
Query Match 34.0%; Score 467.5; DB 5; Length 312;  
Best Local Similarity 43.4%; Pred. No. 4.8e-28;  
RESULT 1352  
ID AAP81243 standard; protein; 247 AA.  
DE Human spleen trypsin III (trypsinogen III).  
PN JP63160582-A.  
PD 04-JUL-1988.  
PA (SANY ) SANKYO CO LTD.  
Query Match 34.0%; Score 467; DB 1; Length 247;  
Best Local Similarity 40.9%; Pred. No. 4.1e-28;  
RESULT 1353  
ID AAR82703 standard; protein; 247 AA.  
DE Human pancreatic trypsin III.  
PN JP07184655-A.  
PD 25-JUL-1995.  
PA (SANY ) SANKYO CO LTD.  
Query Match 34.0%; Score 467; DB 2; Length 247;  
Best Local Similarity 40.9%; Pred. No. 4.1e-28;

RESULT 1354  
ID ADJ59026 standard; protein; 261 AA.  
DE Human PSA analogue (Y154) precursor protein sequence.  
PN W02003047506-A2.  
PD 12-JUN-2003.  
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
Query Match 34.0%; Score 466.5; DB 7; Length 261;  
Best Local Similarity 40.4%; Pred. No. 4.7e-28;  
RESULT 1355  
ID ABB84422 standard; peptide; 226 AA.  
DE Rat SCCE protein N-terminal fragment SEQ ID 48.  
PN W0200262135-A2.  
PD 15-AUG-2002.  
PA (EGEL/) EGELRUD T.  
PA (HANS/) HANSSON L.  
Query Match 33.8%; Score 464.5; DB 5; Length 226;  
Best Local Similarity 42.7%; Pred. No. 5.8e-28;  
RESULT 1356  
ID ADJ59028 standard; protein; 261 AA.  
DE Human PSA analogue (L155/Y154) precursor protein sequence.  
PN W02003047506-A2.  
PD 12-JUN-2003.  
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
Query Match 33.8%; Score 464.5; DB 7; Length 261;  
Best Local Similarity 40.4%; Pred. No. 6.8e-28;  
RESULT 1357  
ID ADA50549 standard; protein; 237 AA.  
DE Rhesus macaque prostate specific antigen (PSA/KLK3), SEQ ID NO:4.  
PN W02003031569-A2.  
PD 17-APR-2003.  
PA (CENZ ) CENTOCOR INC.  
Query Match 33.8%; Score 464; DB 6; Length 237;  
Best Local Similarity 42.6%; Pred. No. 6.7e-28;  
RESULT 1358  
ID ADM12395 standard; protein; 261 AA.  
DE Human prostate-specific antigen protein.  
PN US2003235594-A1.  
PD 25-DEC-2003.  
PA (ANTI-) ANTIGEN EXPRESS INC.  
Query Match 33.7%; Score 463.5; DB 8; Length 261;  
Best Local Similarity 40.0%; Pred. No. 8.1e-28;  
RESULT 1359  
ID ADR66838 standard; protein; 248 AA.  
DE Human prostatic carcinoma derived DNA SEQ ID 131 #4.  
PN W02004076614-A2.  
PD 10-SEP-2004.  
PA (HINZ/) HINZMANN B.  
PA (DAHL/) DAHL E.  
PA (ROSE/) ROSENTHAL A.  
PA (HERM/) HERMANN K.  
PA (PILA/) PILARSKY C.  
Query Match 33.7%; Score 462.5; DB 8; Length 248;  
Best Local Similarity 40.2%; Pred. No. 9.2e-28;  
RESULT 1360  
ID ADR66277 standard; protein; 248 AA.  
DE Human prostatic carcinoma derived protein SEQ ID 131 #2.  
PN W02004076614-A2.  
PD 10-SEP-2004.  
PA (HINZ/) HINZMANN B.  
PA (DAHL/) DAHL E.  
PA (ROSE/) ROSENTHAL A.  
PA (HERM/) HERMANN K.  
PA (PILA/) PILARSKY C.  
Query Match 33.7%; Score 462.5; DB 8; Length 248;  
Best Local Similarity 40.2%; Pred. No. 9.2e-28;  
RESULT 1361  
ID ADR66934 standard; protein; 251 AA.  
DE Human prostatic carcinoma derived DNA SEQ ID 232 #4.  
PN W02004076614-A2.  
PD 10-SEP-2004.  
PA (HINZ/) HINZMANN B.  
PA (DAHL/) DAHL E.  
PA (ROSE/) ROSENTHAL A.

PA (HERM/) HERMANN K.  
PA (PILA/) PILARSKY C.  
Query Match 33.7%; Score 462.5; DB 8; Length 251;  
Best Local Similarity 40.2%; Pred. No. 9.3e-28;  
RESULT 1362  
ID ADR66036 standard; protein; 251 AA.  
DE Human prostatic carcinoma derived protein SEQ ID 232 #1.  
PN W02004076614-A2.  
PD 10-SEP-2004.  
PA (HINZ/) HINZMANN B.  
PA (DAHL/) DAHL E.  
PA (ROSE/) ROSENTHAL A.  
PA (HERM/) HERMANN K.  
PA (PILA/) PILARSKY C.  
Query Match 33.7%; Score 462.5; DB 8; Length 251;  
Best Local Similarity 40.2%; Pred. No. 9.3e-28;  
RESULT 1363  
ID ADP27546 standard; protein; 281 AA.  
DE Human kallikrein-3 (KLK-3) EHT103 protien b variant SeqID 20.  
PN FR2848569-A1.  
PD 18-JUN-2004.  
PA (EXON-) EXONHIT THERAPEUTICS SA.  
Query Match 33.6%; Score 462; DB 8; Length 281;  
Best Local Similarity 41.0%; Pred. No. 1.1e-27;  
RESULT 1364  
ID ADP27545 standard; protein; 297 AA.  
DE Human kallikrein-3 (KLK-3) EHT103 protien a variant SeqID 19.  
PN FR2848569-A1.  
PD 18-JUN-2004.  
PA (EXON-) EXONHIT THERAPEUTICS SA.  
Query Match 33.6%; Score 462; DB 8; Length 297;  
Best Local Similarity 41.0%; Pred. No. 1.2e-27;  
RESULT 1365  
ID AAR84668 standard; protein; 261 AA.  
DE Prepro-hk2 kallikrein.  
PN W09530758-A1.  
PD 16-NOV-1995.  
PA (MAYO-) MAYO FOUNDATION.  
PA (HYBR-) HYBRITTECH INC.  
Query Match 33.5%; Score 460.5; DB 2; Length 261;  
Best Local Similarity 40.2%; Pred. No. 1.4e-27;  
RESULT 1366  
ID AAW10600 standard; protein; 261 AA.  
DE Human prepro-Trp226-glandular kallikrein-2.  
PN W09701630-A1.  
PD 16-JAN-1997.  
PA (ORIN ) ORION VHTYMAE OY.  
Query Match 33.5%; Score 460.5; DB 2; Length 261;  
Best Local Similarity 40.2%; Pred. No. 1.4e-27;  
RESULT 1367  
ID AAU98921 standard; protein; 245 AA.  
DE Human prostate specific antigen (PSA) variant.  
PN W0200240059-A2.  
PD 23-MAY-2002.  
PA (AMBI-) AMERICAN FOUND BIOLOGICAL RES INC.  
PA (MINC/) MINCHEFF M S.  
PA (LOUK/) LOUKINOV D I.  
PA (ZOUB/) ZOUBAK S.  
Query Match 33.4%; Score 459.5; DB 5; Length 245;  
Best Local Similarity 41.4%; Pred. No. 1.5e-27;  
RESULT 1368  
ID AAY08894 standard; protein; 238 AA.  
DE Chimeric serine protease FXT protein.  
PN EP927764-A2.  
PD 07-JUL-1999.  
PA (HOFF ) ROCHE DIAGNOSTICS GMBH.  
Query Match 33.4%; Score 459; DB 2; Length 238;  
Best Local Similarity 40.5%; Pred. No. 1.6e-27;  
RESULT 1369  
ID AAB21314 standard; protein; 255 AA.  
DE Human KLK2.  
PN W0200053776-A2.  
PD 14-SEP-2000.

PA (MOUN ) MOUNT SINAI HOSPITAL.  
Query Match 33.4%; Score 458.5; DB 3; Length 255;  
Best Local Similarity 40.8%; Pred. No. 1.9e-27;  
RESULT 1370  
ID AAW6971 standard; protein; 261 AA.  
DE Prostate-specific glandular kallikrein prepro-hk2.  
PN W09634964-A2.  
PD 07-NOV-1996.  
PA (HYBR-) HYBRITTECH INC.  
PA (MAYO-) MAYO FOUNDATION.  
Query Match 33.4%; Score 458.5; DB 2; Length 261;  
Best Local Similarity 40.8%; Pred. No. 2e-27;  
RESULT 1371  
ID AAW83203 standard; protein; 261 AA.  
DE Prostate-specific glandular kallikrein protein pbhk2.  
PN W09846795-A1.  
PD 22-OCT-1998.  
PA (BAYU ) BAYLOR COLLEGE MEDICINE.  
PA (MAYO-) MAYO FOUNDATION.  
Query Match 33.4%; Score 458.5; DB 2; Length 261;  
Best Local Similarity 40.8%; Pred. No. 2e-27;  
RESULT 1372  
ID AAW49085 standard; protein; 261 AA.  
DE Wild-type human Kallikrein 2 (hk2).  
PN W09821365-A2.  
PD 22-MAY-1998.  
PA (MAYO-) MAYO FOUNDATION.  
PA (HYBR-) HYBRITTECH INC.  
Query Match 33.4%; Score 458.5; DB 2; Length 261;  
Best Local Similarity 40.8%; Pred. No. 2e-27;  
RESULT 1373  
ID AAW45397 standard; protein; 261 AA.  
DE Prostate-specific glandular kallikrein precursor prepro-hk2.  
PN W09802748-A1.  
PD 22-JAN-1998.  
PA (MAYO-) MAYO FOUNDATION.  
PA (HYBR-) HYBRITTECH INC.  
Query Match 33.4%; Score 458.5; DB 2; Length 261;  
Best Local Similarity 40.8%; Pred. No. 2e-27;  
RESULT 1374  
ID AAW96189 standard; protein; 261 AA.  
DE Prepro human Kallikrein 2 (preprohk2).  
PN W09859073-A1.  
PD 30-DEC-1998.  
PA (MAYO-) MAYO FOUNDATION.  
PA (YOUN/) YOUNG C Y F.  
PA (TIND/) TINDALL D J.  
PA (KLEE/) KLEE G G.  
Query Match 33.4%; Score 458.5; DB 2; Length 261;  
Best Local Similarity 40.8%; Pred. No. 2e-27;  
RESULT 1375  
ID AAB21318 standard; protein; 261 AA.  
DE Human KLK2.  
PN W0200053776-A2.  
PD 14-SEP-2000.  
PA (MOUN ) MOUNT SINAI HOSPITAL.  
Query Match 33.4%; Score 458.5; DB 3; Length 261;  
Best Local Similarity 40.8%; Pred. No. 2e-27;  
RESULT 1376  
ID AAU06279 standard; protein; 261 AA.  
DE Human Kallikrein2 polypeptide.  
PN W0200145728-A2.  
PD 28-JUN-2001.  
PA (EPIM-) EPIMUNE INC.  
Query Match 33.4%; Score 458.5; DB 4; Length 261;  
Best Local Similarity 40.8%; Pred. No. 2e-27;  
RESULT 1377  
ID ADB75390 standard; protein; 261 AA.  
DE Prostate cancer marker protein.  
PN W02003009814-A2.  
PD 08-FEB-2003.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 33.4%; Score 458.5; DB 7; Length 261;

Best Local Similarity 40.8%; Pred. No. 2e-27;  
RESULT 1378  
ID AAW83213 standard; protein; 237 AA.  
DE Prostate-specific antigen protein hk3.  
PN W09846795-A1.  
PD 22-OCT-1998.  
PA (BAYU ) BAYLOR COLLEGE MEDICINE.  
PA (MAYO-) MAYO FOUNDATION.  
Query Match 33.3%; Score 457.5; DB 2; Length 237;  
Best Local Similarity 41.6%; Pred. No. 2.1e-27;  
RESULT 1379  
ID AAW56086 standard; protein; 237 AA.  
DE Human prostate specific antigen protein.  
PN W09810292-A1.  
PD 12-MAR-1998.  
PA (CENZ ) CENTOCOR INC.  
Query Match 33.3%; Score 457.5; DB 2; Length 237;  
Best Local Similarity 41.6%; Pred. No. 2.1e-27;  
RESULT 1380  
ID AAW96187 standard; protein; 237 AA.  
DE Human prostate specific antigen (PSA).  
PN W09859073-A1.  
PD 30-DEC-1998.  
PA (MAYO-) MAYO FOUNDATION.  
PA (YOUN/) YOUNG C Y F.  
PA (TIND/) TINDALL D J.  
PA (KLEE/) KLEE G G.  
Query Match 33.3%; Score 457.5; DB 2; Length 237;  
Best Local Similarity 41.6%; Pred. No. 2.1e-27;  
RESULT 1381  
ID AAB11041 standard; peptide; 237 AA.  
DE Human prostate-specific antigen N-terminal fragment #2.  
PN E1043394-A2.  
PD 11-OCT-2000.  
PA (SERA-) SERATEC GES BIOTECHNOLOGIE MBH.  
Query Match 33.3%; Score 457.5; DB 3; Length 237;  
Best Local Similarity 41.6%; Pred. No. 2.1e-27;  
RESULT 1382  
ID AAB19819 standard; protein; 237 AA.  
DE Prostate specific antigen specific to benign prostatic hyperplasia.  
PN W0200067030-A1.  
PD 09-NOV-2000.  
PA (HYBR-) HYBRITTECH INC.  
PA (BAYU ) BAYLOR COLLEGE MEDICINE.  
Query Match 33.3%; Score 457.5; DB 4; Length 237;  
Best Local Similarity 41.6%; Pred. No. 2.1e-27;  
RESULT 1383  
ID AAB19818 standard; protein; 237 AA.  
DE Prostate specific antigen elevated in benign prostatic hyperplasia.  
PN W0200066718-A1.  
PD 09-NOV-2000.  
PA (HYBR-) HYBRITTECH INC.  
PA (BAYU ) BAYLOR COLLEGE MEDICINE.  
Query Match 33.3%; Score 457.5; DB 4; Length 237;  
Best Local Similarity 41.6%; Pred. No. 2.1e-27;  
RESULT 1384  
ID ADA50546 standard; protein; 237 AA.  
DE Human prostate specific antigen (PSA/KLK3), SEQ ID NO:1.  
PN W02003031569-A2.  
PD 17-APR-2003.  
PA (CENZ ) CENTOCOR INC.  
Query Match 33.3%; Score 457.5; DB 6; Length 237;  
Best Local Similarity 41.6%; Pred. No. 2.1e-27;  
RESULT 1385  
ID ADA09840 standard; protein; 237 AA.  
DE Human mature prostate specific antigen (PSA).  
PN US2003059864-A1.  
PD 27-MAR-2003.  
PA (MIKO/) MIKOLAJCZYK S D.  
PA (RITT/) RITTENHOUSE H G.  
Query Match 33.3%; Score 457.5; DB 6; Length 237;  
Best Local Similarity 41.6%; Pred. No. 2.1e-27;  
RESULT 1386





Best Local Similarity 41.8%; Pred. No. 5.3e-27;  
RESULT 1403  
ID AAW03130 standard; protein; 250 AA.  
DE Prostate-specific antigen.  
PN WO9621042-A2.  
PD 11-JUL-1996.  
PA (UYBO-) UNIV BOSTON.  
Query Match 32.9%; Score 452.5; DB 2; Length 250;  
Best Local Similarity 40.5%; Pred. No. 5.4e-27;  
RESULT 1404  
ID ADP27538 standard; protein; 281 AA.  
DE Human kallikrein-2 (KLK-2) EHT102 protein b variant SeqID 12.  
PN FR2848569-A1.  
PD 18-JUN-2004.  
PA (EXON-) EXONHIT THERAPEUTICS SA.  
Query Match 32.9%; Score 452.5; DB 8; Length 281;  
Best Local Similarity 41.8%; Pred. No. 6.1e-27;  
RESULT 1405  
ID ADP27537 standard; protein; 297 AA.  
DE Human kallikrein-2 (KLK-2) EHT102 protein a variant SeqID 11.  
PN FR2848569-A1.  
PD 18-JUN-2004.  
PA (EXON-) EXONHIT THERAPEUTICS SA.  
Query Match 32.9%; Score 452.5; DB 8; Length 297;  
Best Local Similarity 41.8%; Pred. No. 6.5e-27;  
RESULT 1406  
ID ADJ59029 standard; protein; 236 AA.  
DE Human PSA analogue (LI55/Y154) mature protein sequence.  
PN WO2003047506-A2.  
PD 12-JUN-2003.  
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.  
Query Match 32.9%; Score 451.5; DB 7; Length 236;  
Best Local Similarity 41.6%; Pred. No. 6.1e-27;  
RESULT 1407  
ID AAR77098 standard; protein; 237 AA.  
DE Prostate-specific antigen.  
PN WO9528498-A1.  
PD 26-OCT-1995.  
PA (UYCO) UNIV COLUMBIA NEW YORK.  
Query Match 32.8%; Score 450.5; DB 2; Length 237;  
Best Local Similarity 40.7%; Pred. No. 7.4e-27;  
RESULT 1408  
ID AAW83202 standard; protein; 237 AA.  
DE Prostate-specific glandular kallikrein protein hk2.  
PN WO9846795-A1.  
PD 22-OCT-1998.  
PA (BAYU) BAYLOR COLLEGE MEDICINE.  
PA (MAYO-) MAYO FOUNDATION.  
Query Match 32.8%; Score 450.5; DB 2; Length 237;  
Best Local Similarity 42.0%; Pred. No. 7.4e-27;  
RESULT 1409  
ID AAW45395 standard; protein; 237 AA.  
DE Mature prostate-specific glandular kallikrein hk2.  
PN WO9802748-A1.  
PD 22-JAN-1998.  
PA (MAYO-) MAYO FOUNDATION.  
PA (HYBR-) HYBRITTECH INC.  
Query Match 32.8%; Score 450.5; DB 2; Length 237;  
Best Local Similarity 42.0%; Pred. No. 7.4e-27;  
RESULT 1410  
ID AAW96186 standard; protein; 237 AA.  
DE Mature human Kallikrein 2 (hk2).  
PN WO9859073-A1.  
PD 30-DEC-1998.  
PA (MAYO-) MAYO FOUNDATION.  
PA (YOUNG) YOUNG C Y F.  
PA (TIND/) TINDALL D J.  
PA (KLEE/) KLEE G G.  
Query Match 32.8%; Score 450.5; DB 2; Length 237;  
Best Local Similarity 42.0%; Pred. No. 7.4e-27;  
RESULT 1411  
ID ADA50561 standard; protein; 237 AA.  
DE Kallikrein KLK2, SEQ ID NO:16.

PN WO2003031569-A2.  
PD 17-APR-2003.  
PA (CENZ) CENTOCOR INC.  
Query Match 32.8%; Score 450.5; DB 6; Length 237;  
Best Local Similarity 42.0%; Pred. No. 7.4e-27;  
RESULT 1412  
ID AAR84667 standard; protein; 237 AA.  
DE Mature kallikrein hk2.  
PN WO9530758-A1.  
PD 16-NOV-1995.  
PA (MAYO-) MAYO FOUNDATION.  
PA (HYBR-) HYBRITTECH INC.  
Query Match 32.6%; Score 448.5; DB 2; Length 237;  
Best Local Similarity 42.0%; Pred. No. 1e-26;  
RESULT 1413  
ID ADI17277 standard; protein; 217 AA.  
DE Polypeptide homologous to a human NOVX domain SeqID 813.  
PN WO200268649-A2.  
PD 06-SEP-2002.  
PA (CURA-) CURAGEN CORP.  
Query Match 32.6%; Score 447.5; DB 5; Length 217;  
Best Local Similarity 44.4%; Pred. No. 1.1e-26;  
RESULT 1414  
ID ADI17269 standard; protein; 217 AA.  
DE Polypeptide homologous to a human NOVX domain SeqID 805.  
PN WO200268649-A2.  
PD 06-SEP-2002.  
PA (CURA-) CURAGEN CORP.  
Query Match 32.6%; Score 447.5; DB 5; Length 217;  
Best Local Similarity 44.4%; Pred. No. 1.1e-26;  
RESULT 1415  
ID ADJ83076 standard; protein; 217 AA.  
DE Trypsin protein which is related to human NOVX protein - SEQ ID 67.  
PN US2003170630-A1.  
PD 11-SEP-2003.  
PA (ALSO) ALSOBROOK J P.  
PA (TCHE) TCHERNEV V T.  
PA (LIUX) LIU X.  
PA (SPYT) SPYTEK K A.  
PA (ZERH) ZERHUSEN B D.  
PA (PATT) PATTURAJAN M.  
PA (LEPL) LEPLEY D M.  
PA (BURG) BURGESS C E.  
PA (SHIM) SHIMKETS R A.  
PA (GROS) GROSSE W M.  
PA (SZEK) SZEKERES E S.  
PA (VERN) VERNET C A M.  
PA (LILL) LI L.  
PA (CASM) CASMAN S J.  
PA (BOLD) BOLDOG F L.  
PA (GORM) GORMAN L.  
PA (GANG) GANGOLLI E A.  
PA (FERN) FERNANDES E R.  
PA (RIEG) RIEGER D K.  
PA (EDIN) EDINGER S R.  
PA (GUNT) GUNTHER E.  
PA (MILL) MILLET I.  
PA (SCIO) SCIORE P.  
PA (ELLE) ELLERMAN K.  
PA (MACD) MACDOUGALL J R.  
PA (SMIT) SMITHSON G.  
Query Match 32.6%; Score 447.5; DB 7; Length 217;  
Best Local Similarity 44.4%; Pred. No. 1.1e-26;  
RESULT 1416  
ID AAW83212 standard; protein; 237 AA.  
DE hk2 variant A217V.  
PN WO9846795-A1.  
PD 22-OCT-1998.  
PA (BAYU) BAYLOR COLLEGE MEDICINE.  
PA (MAYO-) MAYO FOUNDATION.  
Query Match 32.6%; Score 447.5; DB 2; Length 237;  
Best Local Similarity 42.0%; Pred. No. 1.3e-26;  
RESULT 1417

ID AAW49087 standard; protein; 237 AA.  
DE Mutant human Kallikrein 2 (hk2) A217V.  
PN WO9821365-A2.  
PD 22-MAY-1998.  
PA (MAYO-) MAYO FOUNDATION.  
PA (HYBR-) HYBRITTECH INC.  
Query Match 32.6%; Score 447.5; DB 2; Length 237;  
Best Local Similarity 42.0%; Pred. No. 1.3e-26;  
RESULT 1418  
ID AAW61190 standard; protein; 237 AA.  
DE Variant human Kallikrein 2 (hk2).  
PN WO9859073-A1.  
PD 30-DEC-1998.  
PA (MAYO-) MAYO FOUNDATION.  
PA (YOUNG-) YOUNG C Y F.  
PA (TIND/) TINDALL D J.  
PA (KLEE/) KLEE G G.  
Query Match 32.6%; Score 447.5; DB 2; Length 237;  
Best Local Similarity 42.0%; Pred. No. 1.3e-26;  
RESULT 1419  
ID AAW11023 standard; protein; 240 AA.  
DE Human prostate specific antigen.  
PN WO9640754-A1.  
PD 19-DEC-1996.  
PA (TEXA) UNIV TEXAS SYSTEM.  
Query Match 32.4%; Score 445; DB 2; Length 240;  
Best Local Similarity 41.0%; Pred. No. 2e-26;  
RESULT 1420  
ID AAR84671 standard; protein; 237 AA.  
DE Mature kallikrein HK3.  
PN WO9530758-A1.  
PD 16-NOV-1995.  
PA (MAYO-) MAYO FOUNDATION.  
PA (HYBR-) HYBRITTECH INC.  
Query Match 32.4%; Score 444.5; DB 2; Length 237;  
Best Local Similarity 41.1%; Pred. No. 2.1e-26;  
RESULT 1421  
ID ABM82643 standard; protein; 227 AA.  
DE Human diagnostic and therapeutic pproteins SEQ ID NO:2892.  
PN WO2004023973-A2.  
PD 25-MAR-2004.  
PA (INCY-) INCYTE CORP.  
Query Match 32.2%; Score 443; DB 8; Length 227;  
Best Local Similarity 39.6%; Pred. No. 2.7e-26;  
RESULT 1422  
ID AAR84670 standard; protein; 238 AA.  
DE Mature kallikrein HK2.  
PN WO9530758-A1.  
PD 16-NOV-1995.  
PA (MAYO-) MAYO FOUNDATION.  
PA (HYBR-) HYBRITTECH INC.  
Query Match 32.1%; Score 441.5; DB 2; Length 238;  
Best Local Similarity 40.9%; Pred. No. 3.6e-26;  
RESULT 1423  
ID AAR94526 standard; protein; 279 AA.  
DE Korean Viper Salmosa thrombin-like protease, Halybin.  
PN EP707067-A2.  
PD 17-APR-1996.  
PA (MOGA-) MOGAM BIOTECHNOLOGY RES INST.  
Query Match 32.0%; Score 439; DB 2; Length 279;  
Best Local Similarity 37.7%; Pred. No. 6.7e-26;  
RESULT 1424  
ID AAG79000 standard; protein; 233 AA.  
DE Mamushi fibrinolytic enzyme, brevinase.  
PN KR2001045716-A.  
PD 05-JUN-2001.  
PA (LEEJ/) LEE J W.  
PA (PARK/) PARK W.  
Query Match 31.8%; Score 436.5; DB 4; Length 233;  
Best Local Similarity 37.9%; Pred. No. 8.7e-26;  
RESULT 1425  
ID AAW52944 standard; protein; 260 AA.  
DE Agkistrodon halys brevicaudus thrombin-like protease, salmobin.

PN KR98002267-A.  
PD 30-MAR-1998.  
PA (MOKA-) MOKAM BIOTECHNOLOGY RES INST.  
Query Match 31.7%; Score 436; DB 2; Length 260;  
Best Local Similarity 36.1%; Pred. No. 1.1e-25;  
RESULT 1426  
ID AAB50447 standard; protein; 205 AA.  
DE Human prostate cancer-related intracellular protein #1.  
PN WO200071711-A2.  
PD 30-NOV-2000.  
PA (SPAT/) SPATCIOGLU F.  
Query Match 31.4%; Score 431.5; DB 4; Length 205;  
Best Local Similarity 44.2%; Pred. No. 1.8e-25;  
RESULT 1427  
ID ADE78966 standard; protein; 227 AA.  
DE Human protein modification and maintenance molecule (PMWM) -4.  
PN WO2003063688-A2.  
PD 07-AUG-2003.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match 31.3%; Score 430; DB 7; Length 227;  
Best Local Similarity 39.2%; Pred. No. 2.7e-25;  
RESULT 1428  
ID AAW69388 standard; protein; 205 AA.  
DE Prostate tumour specific gene clone DE13 protein.  
PN WO9837418-A2.  
PD 27-AUG-1998.  
PA (CORI-) CORIXA CORP.  
Query Match 31.0%; Score 426.5; DB 2; Length 205;  
Best Local Similarity 43.7%; Pred. No. 4.5e-25;  
RESULT 1429  
ID AAW71872 standard; protein; 205 AA.  
DE Protein encoded by prostate tumour clone P703 splice variant DE13.  
PN WO9837093-A2.  
PD 27-AUG-1998.  
PA (CORI-) CORIXA CORP.  
Query Match 31.0%; Score 426.5; DB 2; Length 205;  
Best Local Similarity 43.7%; Pred. No. 4.5e-25;  
RESULT 1430  
ID AAY82005 standard; protein; 205 AA.  
DE Human immunogenic prostate tumour protein sequence SEQ ID NO:176.  
PN WO200004149-A2.  
PD 27-JAN-2000.  
PA (CORI-) CORIXA CORP.  
Query Match 31.0%; Score 426.5; DB 3; Length 205;  
Best Local Similarity 43.7%; Pred. No. 4.5e-25;  
RESULT 1431  
ID ASG94414 standard; protein; 205 AA.  
DE Human prostate tumour protein partial variant sequence #2.  
PN US2002090372-A1.  
PD 11-JUL-2002.  
PA (XUJ/) XU J.  
PA (DILL/) DILLON D C.  
Query Match 31.0%; Score 426.5; DB 3; Length 205;  
Best Local Similarity 43.7%; Pred. No. 4.5e-25;  
RESULT 1432  
ID AAM01120 standard; protein; 205 AA.  
DE Human prostate-specific amino acid sequence P703P-DE13.  
PN WO200151633-A2.  
PD 19-JUL-2001.  
PA (CORI-) CORIXA CORP.  
Query Match 31.0%; Score 426.5; DB 4; Length 205;  
Best Local Similarity 43.7%; Pred. No. 4.5e-25;  
RESULT 1433  
ID AAU69766 standard; protein; 205 AA.  
DE Human prostate cDNA encoded protein #6.  
PN WO200173032-A2.  
PD 04-OCT-2001.  
PA (CORI-) CORIXA CORP.  
Query Match 31.0%; Score 426.5; DB 4; Length 205;  
Best Local Similarity 43.7%; Pred. No. 4.5e-25;  
RESULT 1434  
ID AAB74803 standard; protein; 205 AA.  
DE Prostate tumour antigen predicted amino acid sequence for P703P-DE13.

PN W0200125272-A2.  
PD 12-APR-2001.  
PA (CORI-) CORIXA CORP.  
Query Match 31.0%; Score 426.5; DB 4; Length 205;  
Best Local Similarity 43.7%; Pred. No. 4.5e-25;  
RESULT 1435  
ID AAG99005 standard; protein; 205 AA.  
DE Human prostate-specific amino acid sequence P703P-DE13.  
PN W0200134802-A2.  
PD 17-MAY-2001.  
PA (CORI-) CORIXA CORP.  
Query Match 31.0%; Score 426.5; DB 4; Length 205;  
Best Local Similarity 43.7%; Pred. No. 4.5e-25;  
RESULT 1436  
ID ASU71656 standard; protein; 205 AA.  
DE Prostate cancer specific antigen P703P #2.  
PN US2002192763-A1.  
PD 19-DEC-2002.  
PA (XUJJ/) XU J.  
PA (DILL/) DILLON D C.  
PA (MITC/) MITCHAM J L.  
PA (HARL/) HARLOCKER S L.  
PA (JIAN/) JIANG Y.  
PA (KALO/) KALOS M D.  
PA (FANG/) FANGER G R.  
PA (RETT/) RETTER M W.  
PA (STOL/) STOLK J A.  
PA (DAYC/) DAY C H.  
PA (VEDV/) VEDVICK T S.  
PA (CART/) CARTER D.  
PA (LISX/) LI S X.  
PA (WANG/) WANG A.  
PA (SKEI/) SKEIKY Y A W.  
PA (HEPL/) HEPLER W T.  
PA (HEND/) HENDERSON R A.  
PA (HURA/) HURAL J.  
PA (MCNE/) MCNEILL P D.  
PA (HOUG/) HOUGHTON R L.  
PA (DBAS/) Y DE BASSOLS C V.  
PA (FOYT/) FOY T M.  
Query Match 31.0%; Score 426.5; DB 4; Length 205;  
Best Local Similarity 43.7%; Pred. No. 4.5e-25;  
RESULT 1437  
ID AAU04964 standard; protein; 205 AA.  
DE Human prostate tumour protein DE13.  
PN US6262245-B1.  
PD 17-JUL-2001.  
PA (CORI-) CORIXA CORP.  
Query Match 31.0%; Score 426.5; DB 4; Length 205;  
Best Local Similarity 43.7%; Pred. No. 4.5e-25;  
RESULT 1438  
ID ABB95225 standard; protein; 205 AA.  
DE Human P703P-DE13 protein SEQ ID NO 176.  
PN US2002022248-A1.  
PD 21-FEB-2002.  
PA (XUJJ/) XU J.  
PA (DILL/) DILLON D C.  
PA (MITC/) MITCHAM J L.  
PA (HARL/) HARLOCKER S L.  
PA (JIAN/) JIANG Y.  
PA (KALO/) KALOS M D.  
PA (FANG/) FANGER G R.  
PA (RETT/) RETTER M W.  
PA (STOL/) STOLK J A.  
PA (DAYC/) DAY C H.  
PA (VEDV/) VEDVICK T S.  
PA (CART/) CARTER D.  
PA (LISX/) LI S X.  
PA (WANG/) WANG A.  
PA (SKEI/) SKEIKY Y A W.  
PA (HEPL/) HEPLER W T.  
PA (HEND/) HENDERSON R A.  
Query Match 31.0%; Score 426.5; DB 5; Length 205;

Best Local Similarity 43.7%; Pred. No. 4.5e-25;  
RESULT 1439  
ID AG76668 standard; protein; 205 AA.  
DE Prostate tumour protein #6.  
PN US2002081580-A1.  
PD 27-JUN-2002.  
PA (XUJJ/) XU J.  
PA (DILL/) DILLON D C.  
Query Match 31.0%; Score 426.5; DB 5; Length 205;  
Best Local Similarity 43.7%; Pred. No. 4.5e-25;  
RESULT 1440  
ID ABR54337 standard; protein; 205 AA.  
DE Prostate tumour specific protein sequence SEQ ID 176.  
PN W0200289747-A2.  
PD 14-NOV-2002.  
PA (CORI-) CORIXA CORP.  
Query Match 31.0%; Score 426.5; DB 6; Length 205;  
Best Local Similarity 43.7%; Pred. No. 4.5e-25;  
RESULT 1441  
ID ADB13626 standard; protein; 205 AA.  
DE Human prostate specific protein P703P-DE13.  
PN US2003185830-A1.  
PD 02-OCT-2003.  
PA (CORI-) CORIXA CORP.  
Query Match 31.0%; Score 426.5; DB 7; Length 205;  
Best Local Similarity 43.7%; Pred. No. 4.5e-25;  
RESULT 1442  
ID ADG26042 standard; protein; 205 AA.  
DE Human prostate-specific polypeptide #6.  
PN US2003157089-A1.  
PD 21-AUG-2003.  
PA (CORI-) CORIXA CORP.  
Query Match 31.0%; Score 426.5; DB 7; Length 205;  
Best Local Similarity 43.7%; Pred. No. 4.5e-25;  
RESULT 1443  
ID ABB09589 standard; protein; 234 AA.  
DE Deinagkistrodon acutus venom thrombin-like protein (234 residue variant).  
PN CN1181421-A.  
PD 13-MAY-1998.  
PA (SHAN-) SHANGHAI BIO-CHEM INST CHINESE ACAD SCI.  
Query Match 30.7%; Score 422.5; DB 5; Length 234;  
Best Local Similarity 36.4%; Pred. No. 1e-24;  
RESULT 1444  
ID ADK36957 standard; protein; 281 AA.  
DE Novel human polypeptide SeqID9039.  
PN W0200216439-A2.  
PD 28-FEB-2002.  
PA (HYSE-) HYSEQ INC.  
Query Match 30.7%; Score 422.5; DB 5; Length 281;  
Best Local Similarity 39.3%; Pred. No. 1.3e-24;  
RESULT 1445  
ID ASU92024 standard; protein; 218 AA.  
DE Human protein modification and maintenance molecule-4 (PMM-4).  
PN W02003031939-A2.  
PD 17-APR-2003.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match 30.7%; Score 422; DB 6; Length 218;  
Best Local Similarity 37.8%; Pred. No. 1.1e-24;  
RESULT 1446  
ID AAB31579 standard; peptide; 225 AA.  
DE Amino acid sequence of cod trypsin isozymes.  
PN W0200078332-A2.  
PD 28-DEC-2000.  
PA (BJAR/) BJARNASON J B.  
Query Match 30.6%; Score 421; DB 4; Length 225;  
Best Local Similarity 44.3%; Pred. No. 1.3e-24;  
RESULT 1447  
ID ADE15982 standard; protein; 218 AA.  
DE G-coupled protein receptor related polypeptide, SEQ ID No 12.  
PN W0200283841-A2.  
PD 24-OCT-2002.  
PA (CURA-) CURAGEN CORP.  
Query Match 30.6%; Score 420; DB 7; Length 218;

Best Local Similarity 37.8%; Pred. No. 1.5e-24;  
Query Match  
RESULT 1448  
ID ADL93921 standard; protein; 218 AA.  
DE Human G-coupled protein receptor-related protein #6.  
PN US2004006205-A1.  
PD 08-JAN-2004.  
PA (LILL//) LI L.  
PA (GERL//) GERLACH V.  
PA (LIUX//) LIU X.  
PA (MILL//) MILLER C E.  
PA (SPYT//) SPYTEK K A.  
PA (ZERH//) ZERHUSEN B D.  
PA (PENA//) PENNA C E A.  
PA (SHEN//) SHENOY S G.  
PA (ZHON//) ZHONG H.  
PA (SMIT//) SMITHSON G.  
PA (CASM//) CASHMAN S J.  
PA (BOLD//) BOLDOG F L.  
PA (VOSS//) VOSS E Z.  
PA (VERN//) VERNET C A.  
PA (MACD//) MACDOUGALL J R.  
PA (RAST//) RASTELLI L.  
PA (ANDE//) ANDERSON D W.  
PA (ZHON//) ZHONG M.  
PA (MEZE//) MEZES P S.  
PA (FURT//) FURTAK K.  
PA (PATT//) PATTURAJAN M.  
PA (BURG//) BURGESS C E.  
PA (MALY//) MALYANKAR U M.  
PA (SHIM//) SHIMKETS R A.  
PA (TAUP//) TAUPIER R J.  
PA (EDIN//) EDINGER S.  
PA (MAZU//) MAZUR A.  
Query Match  
Best Local Similarity 30.6%; Score 420; DB 8; Length 218;  
RESULT 1449  
ID AAY28641 standard; protein; 207 AA.  
DE Human secreted protein from cDNA clone HKAET41.  
PN WO9940183-A1.  
PD 12-AUG-1999.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match  
Best Local Similarity 30.4%; Score 418; DB 2; Length 207;  
RESULT 1450  
ID AA46773 standard; protein; 233 AA.  
DE Amino acid sequence of Salmonase.  
PN EF814164-A2.  
PD 29-DEC-1997.  
PA (MOGA-) MOGAM BIOTECHNOLOGY RES INST.  
Query Match  
Best Local Similarity 36.6%; Pred. No. 2.5e-24;  
RESULT 1451  
ID AAE21442 standard; protein; 226 AA.  
DE Human trypsin domain consensus protein #2.  
PN WO200226802-A2.  
PD 04-APR-2002.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match  
Best Local Similarity 30.3%; Score 416.5; DB 5; Length 226;  
RESULT 1452  
ID ABG75786 standard; protein; 226 AA.  
DE Trypsin domain consensus sequence, SMART.  
PN US2002165152-A1.  
PD 07-NOV-2002.  
PA (KAPE//) KAPPELLER-LIBERWANN R.  
Query Match  
Best Local Similarity 30.3%; Score 416.5; DB 6; Length 226;  
RESULT 1453  
ID ADA05736 standard; protein; 198 AA.  
DE Human NOV18c protein SEQ ID NO:96.  
PN WO2003029424-A2.  
PD 10-APR-2003.  
PA (CURA-) CURAGEN CORP.

Query Match  
Best Local Similarity 30.0%; Score 412.5; DB 6; Length 198;  
RESULT 1454  
ID ADN62900 standard; protein; 198 AA.  
DE Human NOV18c.  
PN US2004038223-A1.  
PD 26-FEB-2004.  
PA (SMIT//) SMITHSON G.  
PA (MILL//) MILLET I.  
PA (PEYM//) PEYMAN J A.  
PA (KEKU//) KEKUDA R.  
PA (JUJJ//) JU J.  
PA (LILL//) LI L.  
PA (GUOX//) GUO X.  
PA (PATT//) PATTURAJAN M.  
PA (SPYT//) SPYTEK K A.  
PA (EDIN//) EDINGER S R.  
PA (ELLE//) ELLERMAN K.  
PA (MALY//) MALYANKAR U M.  
PA (ORTT//) ORT T.  
PA (GORM//) GORMAN L.  
PA (ZERH//) ZERHUSEN B D.  
PA (ANDE//) ANDERSON D W.  
PA (ZHON//) ZHONG M.  
PA (CATT//) CATTERTON E.  
PA (JIWW//) JI W.  
PA (MILL//) MILLER C E.  
PA (RAST//) RASTELLI L.  
PA (STON//) STONE D J.  
PA (PENA//) PENNA C E A.  
PA (SHEN//) SHENOY S G.  
PA (SHIM//) SHIMKETS R A.  
PA (ROTH//) ROTHENBERG M E.  
PA (LEAC//) LEACH M D.  
PA (AGEE//) AGE E M L.  
PA (BERG//) BERGHS C.  
PA (DIPI//) DIPIPPPO V A.  
PA (EISE//) EISEN A.  
PA (GANG//) GANGOLLI E A.  
PA (RIEG//) RIEGER D K.  
PA (SPAD//) SPADERNA S K.  
Query Match  
Best Local Similarity 30.0%; Score 412.5; DB 8; Length 198;  
RESULT 1455  
ID ADA50560 standard; protein; 194 AA.  
DE Prostate specific antigen (PSA/KLK3), SEQ ID NO:15.  
PN WO2003031569-A2.  
PD 17-APR-2003.  
PA (CENZ-) CENTOCOR INC.  
Query Match  
Best Local Similarity 29.8%; Score 409; DB 6; Length 194;  
RESULT 1456  
ID ADG75684 standard; protein; 215 AA.  
DE Human protein modification and maintenance molecule polypeptide SeqID8.  
PN WO2003083084-A2.  
PD 09-OCT-2003.  
PA (INCY-) INCYTE CORP.  
Query Match  
Best Local Similarity 29.8%; Score 409; DB 7; Length 215;  
RESULT 1457  
ID ABM82829 standard; protein; 215 AA.  
DE Human diagnostic and therapeutic pprotein SEQ ID NO:3078.  
PN WO2004023973-A2.  
PD 25-MAR-2004.  
PA (INCY-) INCYTE CORP.  
Query Match  
Best Local Similarity 29.8%; Score 409; DB 8; Length 215;  
RESULT 1458  
ID ABM83248 standard; protein; 299 AA.  
DE Human diagnostic and therapeutic pprotein SEQ ID NO:3497.  
PN WO2004023973-A2.  
PD 25-MAR-2004.  
PA (INCY-) INCYTE CORP.

Query Match  
Best Local Similarity 29.8%; Score 409; DB 8; Length 299;  
RESULT 1459  
ID ADA05738 standard; protein; 181 AA.  
DE Human NOV18d protein SEQ ID NO:98.  
PN WO2003029424-A2.  
PD 10-APR-2003.  
PA (CURA-) CURAGEN CORP.  
Query Match  
Best Local Similarity 29.7%; Score 408.5; DB 6; Length 181;  
RESULT 1460  
ID ADN62902 standard; protein; 181 AA.  
DE Human NOV18d.  
PN US2004038223-A1.  
PD 26-FEB-2004.  
PA (SMIT/) SMITHSON G.  
PA (MILL/) MILLET I.  
PA (PEYM/) PEYMAN J A.  
PA (KEKU/) KEKUDA R.  
PA (JUUJ/) JU J.  
PA (LILL/) LI L.  
PA (GUOX/) GUO X.  
PA (PATT/) PATTURAJAN M.  
PA (SPYT/) SPYTEK K A.  
PA (EDIN/) EDINGER S R.  
PA (ELLE/) ELLERMAN K.  
PA (NALLY/) MALLYANKAR U M.  
PA (ORTT/) ORT T.  
PA (GORM/) GORMAN L.  
PA (ZERH/) ZERHUSEN B D.  
PA (ANDE/) ANDERSON D W.  
PA (ZHON/) ZHONG M.  
PA (CATT/) CATTERTON E.  
PA (JIWW/) JI W.  
PA (MILL/) MILLER C E.  
PA (RAST/) RASTELLI L.  
PA (STON/) STONE D J.  
PA (PENA/) PENA C E A.  
PA (SHEN/) SHENOY S G.  
PA (SHIM/) SHINKETS R A.  
PA (ROTH/) ROTHENBERG M E.  
PA (LEAC/) LEACH M D.  
PA (AGEE/) AGEE M L.  
PA (BERG/) BERGHS C.  
PA (DIPI/) DIPIPPO V A.  
PA (EISE/) EISEN A.  
PA (GANG/) GANGOLLI E A.  
PA (RIEG/) RIEGER D K.  
PA (SPAD/) SPADERNA S K.  
Query Match  
Best Local Similarity 29.7%; Score 408.5; DB 8; Length 181;  
RESULT 1461  
ID ABM82641 standard; protein; 222 AA.  
DE Human diagnostic and therapeutic pprotein SEQ ID NO:2890.  
PN WO2004023973-A2.  
PD 25-MAR-2004.  
PA (INCY-) INCYTE CORP.  
Query Match  
Best Local Similarity 29.6%; Score 407; DB 8; Length 222;  
RESULT 1462  
ID AAB08510 standard; protein; 230 AA.  
DE A recombinant protein C activator polypeptide.  
PN WO200050612-A2.  
PD 31-AUG-2000.  
PA (INLI-) INSTRUMENTATION LAB.  
Query Match  
Best Local Similarity 29.6%; Score 406.5; DB 3; Length 230;  
RESULT 1463  
ID AAW76538 standard; protein; 231 AA.  
DE A contortrix protein C activator protein fragment.  
PN WO9842850-A1.  
PD 01-OCT-1998.  
PA (RPMS-) RPMS TECHNOLOGY LTD.

Query Match  
Best Local Similarity 29.8%; Score 409; DB 8; Length 299;  
RESULT 1459  
ID ADA05738 standard; protein; 181 AA.  
DE Human NOV18d protein SEQ ID NO:98.  
PN WO2003029424-A2.  
PD 10-APR-2003.  
PA (CURA-) CURAGEN CORP.  
Query Match  
Best Local Similarity 29.7%; Score 408.5; DB 6; Length 181;  
RESULT 1460  
ID ADN62902 standard; protein; 181 AA.  
DE Human NOV18d.  
PN US2004038223-A1.  
PD 26-FEB-2004.  
PA (SMIT/) SMITHSON G.  
PA (MILL/) MILLET I.  
PA (PEYM/) PEYMAN J A.  
PA (KEKU/) KEKUDA R.  
PA (JUUJ/) JU J.  
PA (LILL/) LI L.  
PA (GUOX/) GUO X.  
PA (PATT/) PATTURAJAN M.  
PA (SPYT/) SPYTEK K A.  
PA (EDIN/) EDINGER S R.  
PA (ELLE/) ELLERMAN K.  
PA (NALLY/) MALLYANKAR U M.  
PA (ORTT/) ORT T.  
PA (GORM/) GORMAN L.  
PA (ZERH/) ZERHUSEN B D.  
PA (ANDE/) ANDERSON D W.  
PA (ZHON/) ZHONG M.  
PA (CATT/) CATTERTON E.  
PA (JIWW/) JI W.  
PA (MILL/) MILLER C E.  
PA (RAST/) RASTELLI L.  
PA (STON/) STONE D J.  
PA (PENA/) PENA C E A.  
PA (SHEN/) SHENOY S G.  
PA (SHIM/) SHINKETS R A.  
PA (ROTH/) ROTHENBERG M E.  
PA (LEAC/) LEACH M D.  
PA (AGEE/) AGEE M L.  
PA (BERG/) BERGHS C.  
PA (DIPI/) DIPIPPO V A.  
PA (EISE/) EISEN A.  
PA (GANG/) GANGOLLI E A.  
PA (RIEG/) RIEGER D K.  
PA (SPAD/) SPADERNA S K.  
Query Match  
Best Local Similarity 29.7%; Score 408.5; DB 8; Length 181;  
RESULT 1461  
ID ABM82641 standard; protein; 222 AA.  
DE Human diagnostic and therapeutic pprotein SEQ ID NO:2890.  
PN WO2004023973-A2.  
PD 25-MAR-2004.  
PA (INCY-) INCYTE CORP.  
Query Match  
Best Local Similarity 29.6%; Score 407; DB 8; Length 222;  
RESULT 1462  
ID AAB08510 standard; protein; 230 AA.  
DE A recombinant protein C activator polypeptide.  
PN WO200050612-A2.  
PD 31-AUG-2000.  
PA (INLI-) INSTRUMENTATION LAB.  
Query Match  
Best Local Similarity 29.6%; Score 406.5; DB 3; Length 230;  
RESULT 1463  
ID AAW76538 standard; protein; 231 AA.  
DE A contortrix protein C activator protein fragment.  
PN WO9842850-A1.  
PD 01-OCT-1998.  
PA (RPMS-) RPMS TECHNOLOGY LTD.

Query Match  
Best Local Similarity 29.6%; Score 406.5; DB 2; Length 231;  
RESULT 1464  
ID ABB09590 standard; protein; 218 AA.  
DE Deinagkistodon acutus venom thrombin-like protein (218 residue variant).  
PN CN1181421-A.  
PD 13-MAR-1998.  
PA (SHAN-) SHANGHAI BIO-CHEM INST CHINESE ACAD SCI.  
Query Match  
Best Local Similarity 29.5%; Score 405.5; DB 5; Length 218;  
RESULT 1465  
ID ABM84665 standard; protein; 220 AA.  
DE Human diagnostic and therapeutic pprotein SEQ ID NO:4914.  
PN WO2004023973-A2.  
PD 25-MAR-2004.  
PA (INCY-) INCYTE CORP.  
Query Match  
Best Local Similarity 29.5%; Score 405; DB 8; Length 220;  
RESULT 1466  
ID AAB08511 standard; protein; 230 AA.  
DE Biosynthetic variant of protein C activator polypeptide.  
PN WO200050612-A2.  
PD 31-AUG-2000.  
PA (INLI-) INSTRUMENTATION LAB.  
Query Match  
Best Local Similarity 29.4%; Score 403.5; DB 3; Length 230;  
RESULT 1467  
ID AAR20557 standard; protein; 234 AA.  
DE Fibrinogenolytic protein #4 from snake venom.  
PN DB4023699-A.  
PD 30-JAN-1992.  
PA (BADI-) BASF AG.  
Query Match  
Best Local Similarity 29.3%; Score 403; DB 2; Length 234;  
RESULT 1468  
ID AAP81333 standard; protein; 255 AA.  
DE Batroxobin.  
PN JP63049084-A.  
PD 01-MAR-1988.  
PA (YAMA/) YAMASHINA I.  
Query Match  
Best Local Similarity 29.3%; Score 402; DB 1; Length 255;  
RESULT 1469  
ID AAR05436 standard; protein; 255 AA.  
DE Batroxobin gene product.  
PN JP02124032-A.  
PD 11-MAY-1990.  
PA (FUJI-) FUJISAWA PHARM CO LTD.  
Query Match  
Best Local Similarity 29.3%; Score 402; DB 2; Length 255;  
RESULT 1470  
ID AAY17869 standard; protein; 255 AA.  
DE Araraca batroxobin.  
PN WO9929838-A1.  
PD 17-JUN-1999.  
PA (BRIM-) BRISTOL-MYERS SQUIBB CO.  
Query Match  
Best Local Similarity 29.3%; Score 402; DB 2; Length 255;  
RESULT 1471  
ID AAE21441 standard; protein; 249 AA.  
DE Human trypsin domain consensus protein #1.  
PN WO200226802-A2.  
PD 04-APR-2002.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match  
Best Local Similarity 29.3%; Score 401.5; DB 5; Length 249;  
RESULT 1472  
ID AAM52946 standard; protein; 231 AA.  
DE Batroxobin, a snake venom protease.  
PN KE98002267-A.  
PD 30-MAR-1998.  
PA (MOKA-) MOKAM BIOTECHNOLOGY RES INST.  
Query Match  
Best Local Similarity 29.1%; Score 400; DB 2; Length 231;

Best Local Similarity 34.2%; Pred. No. 5.6e-23;  
RESULT 1473  
ID AAB11711 standard; protein; 264 AA.  
DE Mouse serine protease BSSP5 (MBSSP5) SEQ ID NO:4.  
PN W0200031243-A1.  
PD 02-JUN-2000.  
PA (FUSO) FUSO PHARM IND LTD.  
Query Match 28.8%; Score 395.5; DB 3; Length 264;  
Best Local Similarity 39.1%; Pred. No. 1.4e-22;  
RESULT 1474  
ID AAM52945 standard; protein; 236 AA.  
DE Flaboboxin, a snake venom protease.  
PN KR98002267-A.  
PD 30-MAR-1998.  
PA (MOKA-) MOKA BIOTECHNOLOGY RES INST.  
Query Match 28.7%; Score 394; DB 2; Length 236;  
Best Local Similarity 36.8%; Pred. No. 1.7e-22;  
RESULT 1475  
ID AAR20556 standard; protein; 236 AA.  
DE Fibrinogenolytic protein #3 from snake venom.  
PN D24023699-A.  
PD 30-JAN-1992.  
PA (BADI) BASP AG.  
Query Match 28.6%; Score 393; DB 2; Length 236;  
Best Local Similarity 37.3%; Pred. No. 2e-22;  
RESULT 1476  
ID ABM82831 standard; protein; 233 AA.  
DE Human diagnostic and therapeutic pprotein SEQ ID NO:3080.  
PN W02004023973-A2.  
PD 25-MAR-2004.  
PA (INCY-) INCYTE CORP.  
Query Match 28.5%; Score 392; DB 8; Length 233;  
Best Local Similarity 36.8%; Pred. No. 2.3e-22;  
RESULT 1477  
ID AAE39993 standard; protein; 253 AA.  
DE Human adipsin protein #2.  
PN US2003092620-A1.  
PD 15-MAY-2003.  
PA (GEST) GENSET SA.  
Query Match 28.5%; Score 391; DB 7; Length 253;  
Best Local Similarity 38.0%; Pred. No. 3e-22;  
RESULT 1478  
ID ABG75785 standard; protein; 227 AA.  
DE Trypsin domain consensus sequence, PFAM.  
PN US2002165152-A1.  
PD 07-NOV-2002.  
PA (KAPE/) KAPPELLER-LIBERMANN R.  
Query Match 28.3%; Score 389; DB 6; Length 227;  
Best Local Similarity 40.4%; Pred. No. 3.9e-22;  
RESULT 1479  
ID ADE58223 standard; protein; 253 AA.  
DE Human Protein P00746, SEQ ID NO 4094.  
PN W02003016475-A2.  
PD 27-FEB-2003.  
PA (GEHO) GEN HOSPITAL CORP.  
PA (FARB) BAYER AG.  
Query Match 28.3%; Score 389; DB 7; Length 253;  
Best Local Similarity 38.5%; Pred. No. 4.3e-22;  
RESULT 1480  
ID AAP70758 standard; protein; 269 AA.  
DE P1g pancreas elastase-2.  
PN JP62000276-A.  
PD 06-JAN-1987.  
PA (SANY) SANKYO CO LTD.  
Query Match 28.2%; Score 388; DB 1; Length 269;  
Best Local Similarity 38.5%; Pred. No. 5.5e-22;  
RESULT 1481  
ID AAE39992 standard; protein; 253 AA.  
DE Human adipsin protein #1.  
PN US2003092620-A1.  
PD 15-MAY-2003.  
PA (GEST) GENSET SA.  
Query Match 28.2%; Score 387; DB 7; Length 253;

Best Local Similarity 38.5%; Pred. No. 6.2e-22;  
RESULT 1482  
ID AAB11710 standard; protein; 264 AA.  
DE Human serine protease BSSP5 (hBSSP5) SEQ ID NO:2.  
PN W0200031243-A1.  
PD 02-JUN-2000.  
PA (FUSO) FUSO PHARM IND LTD.  
Query Match 28.1%; Score 386.5; DB 3; Length 264;  
Best Local Similarity 36.8%; Pred. No. 7e-22;  
RESULT 1483  
ID ABR39439 standard; protein; 264 AA.  
DE Human GENSET polypeptide clone name vCTRL-1.  
PN W02003014151-A2.  
PD 20-FEB-2003.  
PA (GEST) GENSET SA.  
Query Match 28.1%; Score 386.5; DB 6; Length 264;  
Best Local Similarity 36.8%; Pred. No. 7e-22;  
RESULT 1484  
ID ABU09382 standard; protein; 271 AA.  
DE Consensus sequence of trypsin-like domain.  
PN W02003031463-A2.  
PD 17-APR-2003.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 28.1%; Score 386; DB 6; Length 271;  
Best Local Similarity 39.1%; Pred. No. 7.9e-22;  
RESULT 1485  
ID ABM82830 standard; protein; 212 AA.  
DE Human diagnostic and therapeutic pprotein SEQ ID NO:3079.  
PN W02004023973-A2.  
PD 25-MAR-2004.  
PA (INCY-) INCYTE CORP.  
Query Match 28.1%; Score 385.5; DB 8; Length 212;  
Best Local Similarity 36.3%; Pred. No. 6.7e-22;  
RESULT 1486  
ID ABM82644 standard; protein; 212 AA.  
DE Human diagnostic and therapeutic pprotein SEQ ID NO:2893.  
PN W02004023973-A2.  
PD 25-MAR-2004.  
PA (INCY-) INCYTE CORP.  
Query Match 28.1%; Score 385.5; DB 8; Length 212;  
Best Local Similarity 36.3%; Pred. No. 6.7e-22;  
RESULT 1487  
ID ABM81778 standard; protein; 264 AA.  
DE Tumour-associated antigenic target (TAT) polypeptide PRO2719, SEQ:4580.  
PN W02004030615-A2.  
PD 15-APR-2004.  
PA (SETH) GENENTECH INC.  
Query Match 28.1%; Score 385.5; DB 8; Length 264;  
Best Local Similarity 36.8%; Pred. No. 8.4e-22;  
RESULT 1488  
ID ADR66037 standard; protein; 213 AA.  
DE Human prostatic carcinoma derived protein SEQ ID 233 #1.  
PN W02004076614-A2.  
PD 10-SEP-2004.  
PA (HINZ/) HINZMANN B.  
PA (DAHL/) DAHL E.  
PA (ROSE/) ROSENTHAL A.  
PA (HERM/) HERMANN K.  
PA (PILA/) PILARSKY C.  
Query Match 28.0%; Score 385; DB 8; Length 213;  
Best Local Similarity 40.2%; Pred. No. 7.4e-22;  
RESULT 1489  
ID ADR66935 standard; protein; 213 AA.  
DE Human prostatic carcinoma derived DNA SEQ ID 233 #4.  
PN W02004076614-A2.  
PD 10-SEP-2004.  
PA (HINZ/) HINZMANN B.  
PA (DAHL/) DAHL E.  
PA (ROSE/) ROSENTHAL A.  
PA (HERM/) HERMANN K.  
PA (PILA/) PILARSKY C.  
Query Match 28.0%; Score 385; DB 8; Length 213;  
Best Local Similarity 40.2%; Pred. No. 7.4e-22;

RESULT 1490  
ID AAP61724 standard; protein; 269 AA.  
DE Porcine elastase II.  
PN JP61192289-A.  
PD 26-AUG-1986.  
PA (KIRI ) KIRIN BREWERY KK.  
Query Match 27.9%; Score 384; DB 1; Length 269;  
Best Local Similarity 38.4%; Pred. No. 1.1e-21;  
RESULT 1491  
ID AAR07513 standard; protein; 258 AA.  
DE Anecd-like polypeptide #2.  
PN EP395375-A.  
PD 31-OCT-1990.  
PA (GLAX ) GLAXO INC.  
PA (KNOL ) KNOLL AG.  
Query Match 27.9%; Score 383; DB 2; Length 258;  
Best Local Similarity 34.3%; Pred. No. 1.3e-21;  
RESULT 1492  
ID AAR05775 standard; protein; 272 AA.  
DE Snake venom anctrod polypeptide.  
PN WO9006362-A.  
PD 14-JUN-1990.  
PA (BADI ) BASF AG.  
PA (BACH/) BACH A.  
Query Match 27.9%; Score 383; DB 2; Length 272;  
Best Local Similarity 33.9%; Pred. No. 1.4e-21;  
RESULT 1493  
ID AAU79393 standard; protein; 171 AA.  
DE Novel human kallikrein KLIK15, splice variant #3.  
PN WO200214485-A2.  
PD 21-FEB-2002.  
PA (MOUN ) MOUNT SINAI HOSPITAL.  
Query Match 27.8%; Score 382.5; DB 5; Length 171;  
Best Local Similarity 35.8%; Pred. No. 9.2e-22;  
RESULT 1494  
ID ADN10933 standard; protein; 171 AA.  
DE Human kallikrein 15, marker of endocrine cancer.  
PN WO2004029285-A2.  
PD 08-APR-2004.  
PA (MOUN ) MOUNT SINAI HOSPITAL.  
Query Match 27.8%; Score 382.5; DB 8; Length 171;  
Best Local Similarity 35.8%; Pred. No. 9.2e-22;  
RESULT 1495  
ID ABM82642 standard; protein; 212 AA.  
DE Human diagnostic and therapeutic pprotein SEQ ID NO:2891.  
PN WO2004023973-A2.  
PD 25-MAR-2004.  
PA (INCY-) INCYTE CORP.  
Query Match 27.8%; Score 382; DB 8; Length 212;  
Best Local Similarity 35.5%; Pred. No. 1.2e-21;  
RESULT 1496  
ID AAR05772 standard; protein; 250 AA.  
DE Human adipisin gene product from the clone phg31.  
PN WO9006365-A.  
PD 14-JUN-1990.  
PA (BETH-) BETH ISRAEL HOSPITAL ASSOC.  
PA (DANA-) DANA-FARBER CANCER INST.  
PA (META-) METABOLIC BIOSYSTEMS INC.  
PA (BETH-) BETH ISRAEL HOSPITAL ASSOC.  
Query Match 27.8%; Score 382; DB 2; Length 250;  
Best Local Similarity 37.2%; Pred. No. 1.5e-21;  
RESULT 1497  
ID AAR05421 standard; protein; 250 AA.  
DE Human adipisin/D encoded by a cDNA.  
PN WO9001540-A.  
PD 22-FEB-1990.  
PA (CALB-) CALIF BIOTECHN INC.  
Query Match 27.8%; Score 382; DB 2; Length 250;  
Best Local Similarity 38.4%; Pred. No. 1.5e-21;  
RESULT 1498  
ID ADE58221 standard; protein; 263 AA.  
DE Rat Protein AAB31922, SEQ ID NO 4092.  
PN WO2003016475-A2.

PD 27-FEB-2003.  
PA (GEHO ) GEN HOSPITAL CORP.  
PA (FARB ) BAYER AG.  
Query Match 27.7%; Score 381; DB 7; Length 263;  
Best Local Similarity 37.6%; Pred. No. 1.9e-21;  
RESULT 1499  
ID ADN9596 standard; protein; 187 AA.  
DE Novel human protein sequence #412.  
PN WO2004038003-A2.  
PD 06-MAY-2004.  
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.  
Query Match 27.6%; Score 379.5; DB 8; Length 187;  
Best Local Similarity 42.7%; Pred. No. 1.7e-21;  
RESULT 1500  
ID ABU92049 standard; protein; 220 AA.  
DE Human protein modification and maintenance molecule-29 (PMNM-29).  
PN WO2003031939-A2.  
PD 17-APR-2003.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match 27.6%; Score 379; DB 6; Length 220;  
Best Local Similarity 37.2%; Pred. No. 2.2e-21;



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OM protein - protein search, using sw model

Run on: March 5, 2005, 17:54:57 ; Search time 174 Seconds  
(without alignments)  
729.860 Million cell updates/sec

Title: US-10-006-856A-194

Perfect score: 1374

Sequence: 1 MGLSIFLLCLVLGLSQAATP.....GVVYICKYVDWIRMIMRN 248

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 1500 summaries

Database : Uniprot\_03.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1374	100.0	248	1	KLKC HUMAN
2	952.5	69.3	234	2	Q9CV76
3	630.5	45.9	260	1	KLK8 HUMAN
4	627.5	45.7	260	2	Q8IW69
5	622.5	45.3	260	1	NRPN MOUSE
6	621.5	45.2	260	1	NRPN RAT
7	618.5	45.0	250	1	KLKB HUMAN
8	611	44.5	255	2	Q7JIG6
9	610	44.4	250	2	Q632P2
10	608	44.3	254	2	Q8CGR4
11	601	43.7	275	2	Q8IXD7
12	599	43.6	255	2	Q6IS10
13	599	43.6	256	1	KLKP HUMAN
14	597.5	43.5	249	2	Q9QVN4
15	597.5	43.5	276	2	Q9OVN3
16	595	43.3	255	2	Q96RQ0
17	588.5	42.8	293	2	Q9D140
18	588	42.8	276	2	Q8CGR6
19	586	42.6	250	2	Q8CGR5
20	578	42.1	242	2	Q8OV54
21	576	41.9	246	2	Q6P320
22	569.5	41.4	248	1	TRY3 CHICK
23	569.5	41.4	251	1	KLKE HUMAN
24	568.5	41.4	251	2	Q6B089
25	568.5	41.4	250	1	KLK9 HUMAN
26	567	41.3	277	1	KLKD HUMAN
27	566	41.2	248	1	TRY2 CHICK
28	565	41.1	248	1	TRY1 CHICK
29	564.5	41.1	293	1	KLK5 HUMAN
30	564	41.0	276	1	KLKA HUMAN
31	563	41.0	244	1	TRY2_XENLA
					P70059 xenopus lae

32	563	41.0	248	2	Q7SZT1	Q7szl1 xenopus lae
33	562	40.9	255	1	Q6GNU2	Q6gnu2 xenopus lae
34	561	40.8	231	1	TRYP_PIG	P00761 sus scrofa
35	561	40.8	243	1	TRY1_BOVIN	P00760 bos taurus
36	561	40.8	244	1	KLK6 HUMAN	Q92876 homo sapien
37	557	40.5	237	2	Q6GYJ5	Q6gyj5 struthio ca
38	555	40.4	243	1	TRY1_XENLA	P19799 xenopus lae
39	555	40.4	243	2	Q7SZ06	Q7sz06 xenopus lae
40	555	40.4	253	1	KLK7 HUMAN	P49862 homo sapien
41	553.5	40.3	246	2	Q88301	Q88301 mus musculus
42	553.5	40.3	253	2	Q91Y82	Q91y82 mus musculus
43	553	40.2	246	1	TRY2_MOUSE	P07146 mus musculus
44	550.5	40.1	247	2	Q9DY77	Q9dy77 mus musculus
45	550	40.0	247	1	TRY2_BOVIN	Q29463 bos taurus
46	549.5	40.0	247	2	Q9CFN9	Q9cfn9 m mus muscu
47	548	39.9	246	2	Q6IE66	Q6ie66 rattus norv
48	546.5	39.8	251	2	O54854	O54854 rattus norv
49	546	39.7	247	1	TRY2_CANFA	P06872 canis famil
50	545	39.7	246	1	TRY1_CANFA	P06871 canis famil
51	544.5	39.6	247	1	TRY3_RAT	P08426 rattus norv
52	544	39.5	246	1	TRY1_RAT	Q8N5N9 homo sapien
53	543	39.5	246	1	TRY1_RAT	P00762 rattus norv
54	543	39.5	246	2	Q792Z1	Q792z1 mus musculus
55	541.5	39.4	247	2	Q9CPN7	Q9cpn7 mus musculus
56	540	39.3	238	1	TRY3_SALSA	P35033 salmo salar
57	540	39.3	246	2	Q792Y8	Q792y8 mus musculus
58	538.5	39.2	249	2	Q91VE3	Q91ve3 m thymopain
59	536	39.0	246	2	Q7TT42	Q7tt42 mus musculus
60	536	39.0	246	2	Q9ROT7	Q9rot7 m pancreati
61	535.5	39.0	245	2	Q6R670	Q6r670 oreochromis
62	535.5	39.0	261	2	Q6H320	Q6h320 bos taurus
63	534.5	38.9	245	2	Q6R671	Q6r671 oreochromis
64	533.5	38.8	245	2	Q792Y9	Q792y9 mus musculus
65	533.5	38.8	247	1	TRY4_RAT	P12798 rattus norv
66	533	38.8	246	1	TRY2_RAT	P00763 rattus norv
67	533	38.8	246	2	Q9ZIR9	Q9zir9 mus musculus
68	532	38.7	246	2	Q9QUR9	Q9qu9 mus musculus
69	528	38.4	246	2	Q792Z0	Q792z0 mus musculus
70	528	38.4	263	2	Q6H319	Q6h319 sus scrofa
71	527.5	38.4	261	1	KLK7_RAT	P36373 rattus norv
72	525	38.2	240	2	Q98TH0	Q98th0 engraulis j
73	523.5	38.1	246	2	Q7M754	Q7m754 mus musculus
74	522	38.0	244	2	Q8QGW3	Q8qgw3 anguilla ja
75	521.5	38.0	246	1	KLK_PIG	P00752 sus scrofa
76	521.5	38.0	261	1	KLK6_MOUSE	P15947 mus musculus
77	520.5	37.9	258	2	Q632F4	Q632f4 rattus norv
78	519	37.8	246	1	TRYA_RAT	P32821 rattus norv
79	518	37.7	246	1	TRYB_RAT	P32822 rattus norv
80	518	37.7	261	1	KLK8_RAT	P36374 rattus norv
81	514.5	37.4	242	2	Q7TIR8	Q7tir8 pangasius h
82	514	37.4	239	2	Q63275	Q63275 rattus norv
83	513.5	37.4	231	1	TRY2_SALSA	P35032 salmo salar
84	513.5	37.4	239	1	KLK2_CAVPO	P12323 cavia porce
85	513.5	37.4	243	2	Q8AV83	Q8av83 brachydanio
86	513.5	37.4	261	2	Q9NIQ1	Q9niqu saguinus oe
87	513.5	37.4	278	2	Q9NM20	Q9nm20 mus musculus
88	512	37.3	279	2	Q6IE55	Q6ie55 rattus norv
89	511.5	37.2	261	2	Q29474	Q29474 canis famil
90	510.5	37.2	238	2	Q9W7Q6	Q9w7q6 paralichthy
91	510.5	37.2	261	1	KLK3_MOUSE	P00756 mus musculus
92	509.5	37.1	222	2	Q8AV11	Q8av11 oncorhynch
93	509.5	37.1	235	2	Q63274	Q63274 rattus norv
94	508	37.0	242	1	TRY1_SALSA	P35031 salmo salar
95	508	37.0	242	2	Q9W7Q7	Q9w7q7 paralichthy
96	507	36.9	244	2	O42159	O42159 petromyzon
97	507	36.9	259	2	Q632F5	Q632f5 rattus norv
98	506	36.8	245	2	O42160	O42160 petromyzon
99	505	36.8	242	2	Q7SX90	Q7sx90 brachydanio
100	505	36.8	249	2	Q92046	Q92046 dissoctich
101	505	36.8	260	1	ESTA_CANFA	P09582 canis famil
102	505	36.8	282	2	Q76B45	Q76b45 blarina bre
103	504.5	36.7	269	2	Q8IU55	Q8iu55 homo sapien
104	503	36.6	241	2	Q98TG9	Q98tg9 engraulis j

105	503	36.6	263	1	KLKR_PRANA	P32824 praomys nat	178	458.5	33.4	261	1	KLK2_HUMAN	P20151 homo sapien
106	502	36.5	249	2	Q9W6K0	Q9W6K0 notothenia	179	452	32.9	260	2	Q71QJ4	Q71QJ4 trimeresuru
107	502	36.5	237	1	KLK3_RAT	P36376 rattus norv	180	451	32.8	260	2	Q7T229	Q7T229 bothrops ja
108	501.5	36.5	259	2	Q91515	Q91515 fugu rubrip	181	450	32.8	260	2	Q8UVX1	Q8UVX1 agkistrodon
109	501	36.5	242	1	Q93266	Q93266 pseudopleur	182	449	32.7	258	1	VSP1_TRIST	Q91516 trimeresuru
110	501	36.5	247	1	TRY2_HUMAN	P07478 homo sapien	183	448	32.6	258	2	Q8AY78	Q8AY78 trimeresuru
111	501	36.5	247	1	Q9W7Q5	Q9W7Q5 paralichthy	184	446.5	32.5	257	2	Q71QI5	Q71QI5 trimeresuru
112	499.5	36.4	241	1	TRYX_GADMO	Q91041 gadus morhu	185	445.5	32.4	257	2	VSP3_TRIMU	Q91509 trimeresuru
113	499	36.3	239	2	Q8N1C9	Q8N1C9 homo sapien	186	444.5	32.4	249	2	Q8JFQ7	Q8JFQ7 gadus morhu
114	498	36.2	249	2	Q788V0	Q788V0 disostichu	187	443	32.2	258	1	VSP2_AKGAC	Q918X1 agkistrodon
115	498	36.2	254	1	KLK4_HUMAN	Q9Y5K2 homo sapien	188	443	32.2	258	1	VSP3_BOTJA	Q9PTU8 bothrops ja
116	497	36.2	257	2	Q61B61	Q61B61 rattus norv	189	439.5	32.0	257	1	VSP7_TRIMU	Q9D9G4 trimeresuru
117	497	36.2	258	1	KLK1_PAPHA	Q28773 papio hamad	190	439	32.0	279	2	Q9YGF8	Q9YGF8 agkistrodon
118	497	36.2	261	2	Q7Z5F4	Q7Z5F4 homo sapien	191	438	31.9	259	1	VSP1_VIPLE	Q9PT41 vipera lebe
119	496.5	36.1	261	1	KLK5_MOUSE	P15945 mus musculu	192	437.5	31.8	257	1	VSP2_TRIMU	Q91508 trimeresuru
120	496	36.1	242	2	Q92099	Q92099 paranotothe	193	437.5	31.8	257	1	VSP4_TRIMU	Q91510 trimeresuru
121	496	36.1	247	2	Q42158	Q42158 petromyzon	194	436.5	31.8	233	2	Q9PT51	Q9PT51 agkistrodon
122	496	36.1	247	2	Q42608	Q42608 petromyzon	195	436.5	31.8	250	2	Q03955	Q03955 praomys nat
123	496	36.1	262	2	Q86U61	Q86U61 homo sapien	196	436.5	31.8	257	1	VSP1_TRIMU	Q91507 trimeresuru
124	495.5	36.1	257	1	KLK1_MACFA	Q07276 macaca fasc	197	436.5	31.8	257	1	VSP5_TRIMU	Q91511 trimeresuru
125	495.5	36.1	261	1	KLK5_MOUSE	P15946 mus musculu	198	435.5	31.7	257	2	Q71QI7	Q71QI7 trimeresuru
126	495	36.0	261	2	Q7Z5F3	Q7Z5F3 homo sapien	199	435	31.7	258	1	VSP2_TRIJE	Q9DF66 trimeresuru
127	495	36.0	261	2	Q6H322	Q6H322 equus cabal	200	434	31.6	258	1	VSP3_TRIJE	Q9DF66 trimeresuru
128	494.5	36.0	247	1	TRY1_HUMAN	P07477 homo sapien	201	434	31.6	260	1	VSPB_TRIGA	Q13061 trimeresuru
129	493.5	35.9	248	2	Q66L05	Q66L05 xenopus lae	202	434	31.6	260	2	Q71QI9	Q71QI9 trimeresuru
130	493	35.9	262	1	KLK1_HUMAN	P06870 homo sapien	203	433.5	31.6	257	2	Q71QJ0	Q71QJ0 trimeresuru
131	492	35.8	262	2	Q66US9	Q66US9 homo sapien	204	433	31.5	260	1	VSP1_AKGHP	Q9YGI2 agkistrodon
132	491.5	35.8	241	1	TRY1_GADMO	P16049 gadus morhu	205	432	31.4	236	1	VSPA_DABRU	P18964 dabola russ
133	491	35.7	256	1	KLK4_MOUSE	P00757 mus musculu	206	432	31.4	257	2	Q9PTL3	Q9PTL3 agkistrodon
134	490.5	35.7	229	1	TRYP_SQUAC	P00764 squalus aca	207	432	31.4	260	1	VSP2_AKGHP	Q9YGI6 agkistrodon
135	490.5	35.6	261	1	KLKD_MOUSE	P36368 mus musculu	208	432	31.4	260	2	Q73800	Q73800 agkistrodon
136	489.5	35.6	261	1	KLKL_MOUSE	P61759 mus musculu	209	431.5	31.4	205	2	Q96JE0	Q96JE0 homo sapien
137	489	35.6	244	1	KLKA_RAT	P36375 rattus norv	210	431.5	31.4	257	2	Q71QJ1	Q71QJ1 trimeresuru
138	488	35.5	247	2	Q8NHM4	Q8NHM4 homo sapien	211	431.5	31.4	261	1	KLK2_HORSE	Q6H321 equus cabal
139	487.5	35.5	251	2	Q9DBQ8	Q9DBQ8 mus musculu	212	431.5	31.4	261	1	KLK2_MOUSE	P04071 mus musculu
140	486	35.4	242	2	Q6RI79	Q6RI79 tautogolabr	213	431	31.4	260	2	VSPA_TRIGA	Q13060 trimeresuru
141	485.5	35.3	234	2	Q9R048	Q9R048 mus musculu	214	431	31.4	260	2	Q8AY81	Q8AY81 trimeresuru
142	485.5	35.3	261	2	O88309	O88309 mus musculu	215	431	31.4	262	1	VSP1_AKGCA	Q91053 agkistrodon
143	484.5	35.3	251	2	O8N2U3	O8N2U3 homo sapien	216	429.5	31.3	205	2	Q96JE2	Q96JE2 homo sapien
144	484.5	35.3	259	1	KLKM_MOUSE	P15948 mus musculu	217	429	31.2	176	2	Q8KSD7	Q8KSD7 mus musculu
145	484.5	35.3	304	1	TRY3_HUMAN	P35030 homo sapien	218	429	31.2	258	1	VSP3_TRIGA	Q13083 trimeresuru
146	484	35.2	255	2	Q9ZDM1	Q9ZDM1 mus musculu	219	429	31.2	260	2	Q71QI0	Q71QI0 trimeresuru
147	483.5	35.2	261	1	KLK1_RAT	P00758 rattus norv	220	428.5	31.2	262	2	Q8QHK3	Q8QHK3 crotalus at
148	483.5	35.2	265	2	Q68G17	Q68G17 rattus norv	221	427	31.1	260	2	Q93502	Q93502 agkistrodon
149	482	35.1	255	2	Q9JIS2	Q9JIS2 mus musculu	222	426.5	31.0	257	1	VSPC_TRIGA	Q13062 trimeresuru
150	481.5	35.0	261	1	KLK3_MOUSE	P15949 mus musculu	223	425	30.9	260	1	VSP1_AKGAC	Q918X2 agkistrodon
151	481	35.0	254	2	Q9XSN6	Q9XSN6 sus scrofa	224	424.5	30.9	257	2	Q71QJ3	Q71QJ3 trimeresuru
152	480.5	35.0	263	1	KLKR_MOUSE	Q9Jm71 mus musculu	225	423	30.8	204	2	Q96JE1	Q96JE1 homo sapien
153	479	34.9	261	1	KLK3_MACMU	P33619 macaca mula	226	423	30.8	238	1	VSP1_AKGHA	P81176 agkistrodon
154	479	34.9	261	2	O6DT45	O6DT45 macaca fasc	227	422.5	30.7	234	2	Q9YGS1	Q9YGS1 agkistrodon
155	478.5	34.8	248	2	O6GPX7	O6GPX7 xenopus lae	228	422.5	30.7	259	2	Q8UUK2	Q8UUK2 crotalus ad
156	478.5	34.8	250	2	Q93265	Q93265 pseudopleur	229	422	30.7	256	2	Q7SYF1	Q7SYF1 cerastes ce
157	477.5	34.8	256	2	Q6IEI2	Q6IEI2 rattus norv	230	421.5	30.7	163	2	Q66H01	Q66H01 xenopus lae
158	477.5	34.8	261	1	KLK1_MOUSE	P00755 mus musculu	231	420.5	30.6	257	2	Q71QI8	Q71QI8 trimeresuru
159	477.5	34.8	263	1	KLKO_MOUSE	Q61754 mus musculu	232	419.5	30.5	234	2	Q8UUK1	Q8UUK1 agkistrodon
160	477	34.7	247	2	Q66PG9	Q66PG9 fugu rubrip	233	419	30.5	258	2	Q8QHK2	Q8QHK2 crotalus at
161	476.5	34.7	344	2	Q9W6J9	Q9W6J9 disostichu	234	418.5	30.5	257	2	Q71QI6	Q71QI6 trimeresuru
162	476.5	34.7	675	2	Q9W6J8	Q9W6J8 disostichu	235	418	30.4	260	2	Q8AY82	Q8AY82 trimeresuru
163	475.5	34.6	219	2	Q91036	Q91036 gadus morhu	236	417	30.3	236	1	VSPC_DABRU	P18965 dabola russ
164	472.5	34.4	235	2	Q66PG8	Q66PG8 fugu rubrip	237	415.5	30.2	178	2	Q93594	Q93594 dicentrarch
165	471	34.3	249	2	Q6DIW2	Q6DIW2 xenopus tro	238	415.5	30.2	257	2	Q71QH8	Q71QH8 trimeresuru
166	470.5	34.2	257	2	Q6LDS3	Q6LDS3 homo sapien	239	414	30.1	237	2	Q8UUK2	Q8UUK2 agkistrodon
167	470.5	34.2	261	1	KLK3_HUMAN	P07288 homo sapien	240	413	30.1	258	1	VSP1_TRIGA	Q13059 trimeresuru
168	470	34.2	258	2	Q71QI1	Q71QI1 trimeresuru	241	413	30.1	258	2	Q7SZE1	Q7SZE1 gloydius sa
169	469.5	34.2	261	1	KLK2_MOUSE	P07628 mus musculu	242	413	30.1	260	1	VSP1_TRIFL	P05620 trimeresuru
170	469.5	34.2	261	2	Q8C232	Q8C232 mus musculu	243	411.5	29.9	280	1	VSPA_LACMU	P33589 lachesis mu
171	468	34.1	259	1	KLK2_RAT	P00759 rattus norv	244	411	29.9	239	2	Q6T5L0	Q6T5L0 gloydius sh
172	467.5	34.0	261	1	KLKQ_MOUSE	P36369 mus musculu	245	411	29.9	258	2	Q71QH7	Q71QH7 trimeresuru
173	467	34.0	258	2	Q71QH6	Q71QH6 trimeresuru	246	411	29.9	260	2	Q7SZC3	Q7SZC3 gallus gall
174	462.5	33.7	261	2	Q8KOC6	Q8KOC6 mus musculu	247	409	29.8	260	1	VSP2_VIPLE	Q9PT40 vipera lebe
175	461.5	33.6	259	1	KLK3_RAT	P07647 rattus norv	248	408.5	29.7	257	2	Q8UH62	Q8UH62 vipera lebe
176	461	33.6	258	2	Q8AY80	Q8AY80 trimeresuru	249	408	29.7	235	1	VSP2_AKGBI	Q9PSN3 agkistrodon
177	458.5	33.4	250	1	TRYP_PLEPL	P35034 pleuronecte	250	407	29.6	237	2	O93421	O93421 agkistrodon

251	407	29.6	258	1	VSP2_AGKCA	O42207 agkistrodon	324	361.5	26.3	267	2	Q7S251	Q7sz51 brachydanio
252	407	29.6	258	2	Q8AY79	O8ay79 trimeresuru	325	361	26.3	255	2	Q6WGR1	Q6wgr1 ictalurus p
253	407	29.6	260	1	VSP2_TRIFL	O13057 trimeresuru	326	361	26.3	267	2	Q640B1	Q640b1 xenopus lae
254	406.5	29.6	231	1	VSP1_AGKCO	P09872 agkistrodon	327	359.5	26.2	259	2	Q6A2C2	Q6azc2 brachydanio
255	406.5	29.6	257	2	Q71QH5	Q71qh5 trimeresuru	328	359.5	26.2	259	2	Q6ISU5	Q6isus anopheles g
256	405.5	29.5	257	2	Q71QI3	Q71qi3 trimeresuru	329	359.5	26.2	277	1	TR12_ANOGA	P35036 anopheles g
257	405	29.5	234	2	Q7S2E2	Q7s2e2 agkistrodon	330	359.5	26.2	342	1	PSS8_MOUSE	Q9esd1 mus musculus
258	403.5	29.4	233	2	Q6IWF1	Q6iwf1 bothrops al	331	359	26.1	265	2	Q6P326	Q6p326 xenopus tro
259	402.5	29.3	232	1	VSP1_BOTJA	P81824 bothrops ja	332	359	26.1	311	2	Q80XZ3	Q80xz3 rattus norv
260	402.5	29.3	257	2	Q9YGF9	O9ygf9 agkistrodon	333	359	26.1	430	2	Q804X0	Q804x0 fugu rubrip
261	402	29.3	255	1	VSPA_BOTAT	P04971 bothrops at	334	358.5	26.1	245	1	MCT1_SHEEP	P80931 ovis aries
262	402	29.3	260	1	VSP1_TRIJE	Q9df68 trimeresuru	335	358.5	26.1	444	1	PA7_RABIT	P98139 oryctolagus
263	402	29.3	260	1	VSP6_TRIMU	Q9d983 trimeresuru	336	358	26.1	812	1	PLMN_BOVIN	P06868 bos taurus
264	400	29.1	234	1	VSP2_AGKCO	P82981 agkistrodon	337	357.5	26.0	232	2	Q9XY45	Q9xy45 ctenocephal
265	400	29.1	258	2	Q802F0	Q802f0 agkistrodon	338	357.5	26.0	371	2	Q8MS52	Q8ms52 drosophila
266	399.5	29.1	257	2	Q8QG86	Q8qg86 bothrops in	339	357.5	26.0	643	2	Q97506	Q97506 sus scrofa
267	399	29.0	260	2	Q71QI2	Q71qi2 trimeresuru	340	357	26.0	262	1	GRAA_HUMAN	P12544 homo sapien
268	397	28.9	235	2	Q90Z47	Q90z47 agkistrodon	341	357	26.0	263	1	CTRB_HUMAN	P17538 homo sapien
269	397	28.9	260	2	Q71QI4	Q71qi4 trimeresuru	342	357	26.0	271	1	CTRL_HUMAN	Q00871 penaeus eu
270	395.5	28.8	264	2	Q9ER05	Q9er05 mus musculus	343	357	26.0	806	1	PLMN_PENVA	O18783 macropus au
271	395	28.7	260	2	Q71QH9	Q71qh9 trimeresuru	344	357	26.0	1019	1	LFC_TACTR	P28175 tachypleus
272	394.5	28.7	257	1	VSP2_BOTJA	O13069 bothrops ja	345	357	26.0	1019	2	Q8T9S1	O8t9s1 tachypleus
273	393.5	28.6	264	2	Q9D7P8	Q9d7p8 mus musculus	346	356.5	25.9	261	2	Q9W7Q4	Q9w7q4 paralichthy
274	393	28.6	260	1	VSP4_AGKAC	Q9i8w5 agkistrodon	347	356.5	25.9	321	1	TRYC_HUMAN	Q9nr22 homo sapien
275	392	28.5	258	2	Q71QI2	Q71qi2 trimeresuru	348	356.5	25.9	321	2	Q96RZ8	Q96rz8 homo sapien
276	391.5	28.5	264	2	Q9EQZ8	Q9eqz8 rattus norv	349	355.5	25.9	260	2	Q9V7G4	Q9v7g4 drosophila
277	391	28.5	253	2	Q8WZB4	Q8wzb4 homo sapien	350	355.5	25.9	276	1	MCT6_MOUSE	P21845 mus musculus
278	389	28.3	253	1	CFAD_HUMAN	P00746 homo sapien	351	355	25.8	342	1	PSS8_RAT	Q9es87 rattus norv
279	389	28.3	258	2	Q8JH85	Q8jh85 vipera lebe	352	354.5	25.8	349	2	Q6OX59	Q6ox59 lepeophthei
280	388.5	28.3	257	1	VSP3_TRIFL	O13058 trimeresuru	353	354.5	25.8	311	2	Q8WZM5	Q8wzm5 trichoderma
281	388	28.2	269	1	EL2_PIG	P08419 sus scrofa	354	354.5	25.8	331	2	Q8RIA6	Q8ria6 mus musculus
282	387	28.2	181	2	Q8NFV7	O8nfv7 homo sapien	355	354.5	25.8	331	2	Q8OX17	Q8ox17 mus musculus
283	387	28.2	243	2	Q8GVJ5	Q8gvj5 homo sapien	356	354	25.8	260	2	Q9W7P9	Q9w7p9 paralichthy
284	387	28.2	258	2	Q98TT5	Q98tt5 agkistrodon	357	354	25.8	271	1	EL2_MOUSE	P05208 mus musculus
285	386.5	28.1	257	1	VSP3_AGKAC	Q9i8x0 agkistrodon	358	353.5	25.7	263	1	CTRA_GADMO	P47796 gadus morhu
286	386	28.1	232	1	VSPA_BOTJA	P81661 bothrops ja	359	353.5	25.7	270	1	TRYT_MERUN	P50342 meriones un
287	386	28.1	258	2	Q91961	Q91961 agkistrodon	360	353.5	25.7	333	2	Q7Q5Z6	Q7q5z6 anopheles g
288	386	28.1	258	2	Q9W7S1	Q9w7s1 agkistrodon	361	353	25.7	274	1	MCT6_RAT	P50343 rattus norv
289	386	28.1	260	2	Q6T6S7	Q6t6s7 bitis gabon	362	353	25.7	314	1	TEST_HUMAN	O9y6m0 homo sapien
290	385.5	28.1	188	1	KLK3_RAT	P15950 rattus norv	363	353	25.7	456	1	PRTC_CANFA	O28278 canis famil
291	385.5	28.1	264	1	CTRL_HUMAN	P40313 homo sapien	364	353	25.7	459	1	PRTC_PIG	Q9gl22 sus scrofa
292	385.5	28.1	264	2	Q9D960	Q9d960 mus musculus	365	352.5	25.7	263	2	Q6PGS4	Q6pgs4 xenopus lae
293	385.5	28.1	269	2	Q8IUW0	Q8iuw0 homo sapien	366	352.5	25.7	321	2	Q6GNK3	Q6gnk3 xenopus lae
294	384.5	28.0	195	2	Q07277	Q07277 homo sapien	367	352	25.6	111	2	Q9UKR2	O9ukr2 homo sapien
295	382.5	27.8	1524	2	Q91674	P191674 xenopus lae	368	352	25.6	260	1	GRAA_MOUSE	P11032 mus musculus
296	381	27.7	263	1	CFAD_RAT	P32038 rattus norv	369	352	25.6	277	2	Q7T0T6	Q7t0t6 xenopus lae
297	380.5	27.7	235	2	Q8N4E0	Q8n4e0 homo sapien	370	352	25.6	304	1	DISP_RAT	P83748 rattus norv
298	380	27.7	157	2	Q6B338	Q6b338 symphysodon	371	352	25.6	505	2	PRCC_MOUSE	Q966v4 halocynthia
299	380	27.7	455	2	Q7SY86	Q7sy86 xenopus lae	372	351.5	25.6	460	1	PRTC_MOUSE	P33587 mus musculus
300	379	27.6	220	2	Q8NCW4	Q8ncw4 homo sapien	373	351	25.5	310	1	DISP_MOUSE	O9qy29 mus musculus
301	378	27.5	261	2	Q6DHD9	Q6dhd9 brachydanio	374	351	25.5	456	1	PRTC_BOVIN	P00745 bos taurus
302	374.5	27.3	259	2	CFAD_MOUSE	P03953 mus musculus	375	350.5	25.5	265	2	Q804G1	Q804g1 brachydanio
303	372.5	27.1	228	2	Q6FHW3	Q6fhw3 homo sapien	376	350.5	25.5	274	2	O16133	O16133 anopheles s
304	372.5	27.1	261	2	Q8CJF4	Q8cjf4 rattus norv	377	350.5	25.5	274	2	Q17086	Q17086 anopheles s
305	371	27.0	271	1	EL2_RAT	P00774 rattus norv	378	350.5	25.5	434	2	Q7T3B6	Q7t3b6 brachydanio
306	370.5	27.0	204	2	Q86VI7	Q86vi7 homo sapien	379	350	25.5	263	2	Q6GP11	Q6gp11 homo sapien
307	370.5	27.0	259	1	CFAD_PIG	P51779 sus scrofa	380	350	25.5	268	2	Q6GOE9	Q6gog9 xenopus lae
308	370.5	27.0	263	1	CTR2_CANFA	P04813 canis famil	381	350	25.5	268	2	Q642S8	Q642s8 xenopus tro
309	370	26.9	234	1	VSP4_AGRKH	P26324 agkistrodon	382	350	25.5	271	2	O18487	O18487 penaeus van
310	370	26.9	270	2	Q819P2	Q819p2 aplysina fi	383	349.5	25.4	261	2	Q66HW9	Q66hw9 brachydanio
311	369	26.9	330	2	Q6NVR7	Q6nvr7 xenopus tro	384	349.5	25.4	269	1	EL2A_HUMAN	P08217 homo sapien
312	368.5	26.8	243	1	PSS8_HUMAN	O16651 homo sapien	385	349.5	25.4	269	2	Q6ICV2	Q6icv2 homo sapien
313	368	26.8	256	1	TRP3_PSEAM	Q93267 pseudopleur	386	349.5	25.4	277	2	O96899	O96899 scolopendra
314	368	26.8	418	1	HATT_HUMAN	O60235 homo sapien	387	349.5	25.4	371	2	Q8CJ16	Q8cj16 rattus norv
315	367.5	26.7	638	1	KAL_HUMAN	P03952 homo sapien	388	349.5	25.4	445	2	Q8CJ17	Q8cj17 rattus norv
316	366	26.6	258	1	VSP2_AGRKH	P47797 agkistrodon	389	349.5	25.4	558	2	Q6L711	Q6l711 rattus norv
317	366	26.6	260	2	Q9W7Q3	O9w7q3 paralichthy	390	349.5	25.4	1130	2	Q7QIM7	Q7qim7 anopheles g
318	365.5	26.6	245	2	Q9XY60	O9xy60 ctenocephal	391	349	25.4	1019	1	LFC_CARRO	Q26422 carlinoscor
319	365	26.6	263	2	Q7SX97	Q7sx97 brachydanio	392	349	25.4	1083	2	Q26423	Q26423 carlinoscor
320	363.5	26.5	339	2	Q9L144	Q9l144 mus musculus	393	348.5	25.4	429	2	Q8AVB0	Q8avb0 brachydanio
321	363	26.4	340	2	Q8BUV6	Q8buv6 mus musculus	394	348.5	25.4	503	2	Q8AYE4	Q8aye4 brachydanio
322	362.5	26.4	246	1	MCT1_MERUN	P50340 meriones un	395	348.5	25.4	799	2	Q6PF94	Q6pf94 mus musculus
323	362.5	26.4	387	2	Q9XY57	O9xy57 ctenocephal	396	348.5	25.4	811	1	TMS6_MOUSE	Q9sdb10 mus musculus

397	348.5	25.4	818	2	Q6PBA6	Q6pba6 brachydanio	470	339.5	24.7	258	1	GRAM RAT	O03238 rattus norv
398	348	25.3	267	1	TRY7 ANOGA	E35041 anopheles g	471	339.5	24.7	271	2	Q803Z4	O803z4 brachydanio
399	348	25.3	269	1	Q61SN8	Q6isn8 homo sapien	472	339.5	24.7	333	1	PLMN_CANFA	P80009 canis fami
400	348	25.3	278	2	Q7PNP6	Q7pnf6 anopheles g	473	339	24.7	321	2	Q61B60	Q61e60 rattus norv
401	347.5	25.3	344	2	Q640F8	Q640f8 xenopus lae	474	339	24.7	335	1	PRTC RABIT	Q28661 oryctolagus
402	347	25.3	275	2	Q6FHB8	Q6fhb8 homo sapien	475	339	24.7	358	1	PRTC RABIT	Q28661 oryctolagus
403	347	25.3	461	1	PRTC HUMAN	P04070 homo sapien	476	339	24.7	461	1	FA9 HUMAN	P00740 homo sapien
404	346.5	25.2	267	2	Q9BK47	Q9bk47 luidia foli	477	339	24.7	461	1	FA9_PANTR	Q95nd7 pan troglod
405	346.5	25.2	269	1	EL2_BOVIN	Q29461 bos taurus	478	339	24.7	625	1	FALL_HUMAN	F03951 homo sapien
406	346.5	25.2	334	2	Q46507	Q46507 papio hamad	479	339	24.7	812	1	PLMN RAT	Q01177 rattus norv
407	346.5	25.2	351	2	Q816K0	Q816k0 holotrichia	480	338.5	24.6	256	2	Q18599	Q18599 drosophila
408	346.5	25.2	435	1	TMS4 MOUSE	Q8vca5 mus musc	481	338.5	24.6	258	1	EL1_HUMAN	Q9unil1 homo sapien
409	346.5	25.2	435	2	Q9NF72	Q9nf72 anopheles g	482	338.5	24.6	258	1	Q867B0	Q867b0 canis fami
410	346.5	25.2	446	1	FA7 MOUSE	P70375 mus muscu	483	338.5	24.6	264	2	Q02569	Q02569 culex quinq
411	346.5	25.2	456	2	Q7QC30	P70375 mus muscu	484	338.5	24.6	307	2	Q6ZND6	Q6znd6 homo sapien
412	346.5	25.2	461	1	PRTC RAT	P70375 mus muscu	485	338.5	24.6	455	2	Q8CDR0	Q8cdr0 mus muscu
413	346.5	25.2	461	2	Q88FY8	Q88fy8 rattus norv	486	338.5	24.6	562	2	Q7PN85	Q7pn85 anopheles g
414	346.5	25.2	612	2	Q804W7	Q804w7 fugu rubrip	487	338.5	24.6	704	1	CRAR MOUSE	P98064 mus muscu
415	346	25.2	311	1	TRYG MOUSE	Q9qu17 mus muscu	488	338.5	24.6	802	2	Q6UXD8	Q6uxd8 homo sapien
416	346	25.2	322	2	Q920S2	Q920s2 mus muscu	489	338	24.6	210	2	Q63Z11	Q63z11 xenopus lae
417	345.5	25.1	454	2	Q46506	Q46506 papio hamad	490	338	24.6	365	2	Q97366	Q97366 holotrichia
418	345.5	25.1	467	2	Q6F7X8	P567x8 panulirus a	491	338	24.6	388	2	Q44330	Q44330 manduca sex
419	345	25.1	253	1	TRYD DROER	P567x8 drosophila	492	338	24.6	418	2	Q7PGU3	Q7pgu3 anopheles g
420	344.5	25.1	117	2	Q9PUF3	Q9puf3 bothrops ja	493	338	24.6	625	1	THRB BOVIN	P00735 bos taurus
421	344.5	25.1	187	2	Q6PK75	Q6pk75 homo sapien	494	337.5	24.6	238	1	TRY5 BDAE	P29787 aedes aegyp
422	344.5	25.1	275	2	Q6B051	Q6b051 homo sapien	495	337.5	24.6	261	2	Q6QX60	Q6qx60 lepeophthei
423	344.5	25.1	855	2	Q7Z410	Q7z410 homo sapien	496	337.5	24.6	264	1	GRAX HUMAN	P49863 homo sapien
424	344.5	25.1	1059	2	Q7Z411	Q7z411 homo sapien	497	337.5	24.6	282	2	Q9D4I3	Q9d4i3 mus muscu
425	344	25.0	257	2	Q8BZ04	Q8bz04 mus muscu	498	337.5	24.6	317	2	Q9DGR3	Q9dgr3 xenopus lae
426	344	25.0	265	2	Q6QX61	Q6qx61 lepeophthei	499	337.5	24.6	328	2	Q80Z40	Q80z40 rattus norv
427	344	25.0	275	1	TRB2 HUMAN	P20231 homo sapien	500	337.5	24.6	432	2	Q6GNA2	Q6gna2 xenopus lae
428	344	25.0	282	2	Q6NZV1	Q6nzv1 homo sapien	501	337.5	24.6	471	2	Q8CFE0	Q8cfe0 mus muscu
429	344	25.0	417	2	Q8BZ10	Q8bz10 mus muscu	502	337	24.5	247	2	Q17039	Q17039 anopheles g
430	343.5	25.0	266	2	Q46644	Q46644 macaca fasc	503	337	24.5	263	2	Q9DBX8	Q9dbx8 mus muscu
431	343.5	25.0	273	1	MCT7 MOUSE	Q02844 mus muscu	504	337	24.5	275	2	Q96RZ6	Q96rz6 homo sapien
432	343.5	25.0	273	2	Q921N4	Q921n4 mus muscu	505	337	24.5	432	2	Q6UX37	Q6ux37 homo sapien
433	343.5	25.0	457	1	TMS5 HUMAN	Q9h383 homo sapien	506	337	24.5	434	1	UROK CHICK	P15120 gallus gall
434	343	25.0	275	1	TRYT CANFA	P15944 canis fami	507	337	24.5	437	1	TMS4 HUMAN	Q9nrs4 homo sapien
435	343	25.0	284	2	Q8NF86	Q8nf86 homo sapien	508	336.5	24.5	247	1	MCT1_PAPHA	P52195 papio hamad
436	343	25.0	318	2	Q7RTY9	Q7rty9 homo sapien	509	336.5	24.5	251	1	MCT3_SHEEP	Q46683 ovis aries
437	342.5	24.9	248	2	Q16126	Q16126 boltentia vi	510	336.5	24.5	280	2	Q6FZV9	Q6fzv9 xenopus tro
438	342.5	24.9	248	2	Q9XY52	Q9xy52 ctenecephal	511	336.5	24.5	329	2	Q42272	Q42272 xenopus lae
439	342.5	24.9	271	2	Q8HYJ2	Q8hyj2 bos taurus	512	336.5	24.5	428	2	Q8WFM7	P26262 mus muscu
440	342.5	24.9	273	1	MCT7 RAT	P27435 rattus norv	513	336.5	24.5	638	1	KAL MOUSE	Q8wpm7 oikopleura
441	342.5	24.9	273	2	Q8P6W8	Q8p6w8 rattus norv	514	336	24.5	227	2	Q8IXI4	Q8ixi4 homo sapien
442	342.5	24.9	433	2	Q8JHD0	Q8jhd0 brachydanio	515	336	24.5	263	2	Q9CR35	Q9cr35 m mus muscu
443	342.5	24.9	433	2	Q90YK1	Q90yk1 brachydanio	516	336	24.5	263	2	Q9DC86	Q9dc86 mus muscu
444	342.5	24.9	517	2	Q8K0D2	Q8k0d2 mus muscu	517	336	24.5	273	1	TRYT_SHEEP	Q9xsm2 ovis aries
445	342.5	24.9	624	1	FALL MOUSE	Q91y47 mus muscu	518	336	24.5	280	2	Q64ID5	Q64id5 anthonomus
446	342.5	24.9	810	1	PLMN HUMAN	P00747 homo sapien	519	336	24.5	402	2	Q7QB73	Q7qb73 anopheles g
447	342.5	24.9	811	1	TMS6 HUMAN	Q8iu80 homo sapien	520	336	24.5	416	1	FA9 BOVIN	P00741 bos taurus
448	342	24.9	275	1	TRB1_HUMAN	Q15661 homo sapien	521	336	24.5	485	2	Q7PKK0	Q7pkk0 anopheles g
449	342	24.9	355	2	Q7PQR9	Q7pqr9 anopheles g	522	336	24.5	556	2	Q803D5	Q803d5 brachydanio
450	342	24.9	812	1	PLMN MOUSE	P20918 mus muscu	523	336	24.5	654	2	Q6QNF4	Q6qnf4 canis fami
451	341.5	24.9	258	1	GRAX RAT	P49864 rattus norv	524	336	24.5	790	1	PLMN_PIG	P06867 sus scrofa
452	341.5	24.9	455	1	TMS5 MOUSE	Q9er04 mus muscu	525	335.5	24.4	258	2	Q6ISM6	Q6iem6 homo sapien
453	341.5	24.9	573	2	Q9V5I6	Q9v5i6 drosophila	526	335.5	24.4	266	1	EL1_BOVIN	Q28153 bos taurus
454	341.5	24.9	1134	2	Q7RTY7	Q7rty7 homo sapien	527	335.5	24.4	275	1	TRYT_PIG	Q9n2d1 sus scrofa
455	341	24.8	251	2	Q9GLN2	Q9gln2 bos taurus	528	335.5	24.4	389	2	Q9PVX7	Q9pvx7 xenopus lae
456	341	24.8	283	2	Q63ZK0	Q63zk0 xenopus lae	529	335.5	24.4	558	2	Q86YM4	Q86ym4 homo sapien
457	341	24.8	388	2	Q61RA4	Q61ra4 xenopus lae	530	335	24.4	216	2	Q9UD19	Q9ud19 homo sapien
458	341	24.8	572	2	Q7RTY8	Q7rty8 homo sapien	531	335	24.4	318	2	Q8MNY6	Q8mny6 nilaparvata
459	341	24.8	719	2	Q6DJ90	Q6dj90 xenopus tro	532	335	24.4	433	2	Q804X5	Q804x5 gallus gall
460	340.5	24.8	246	1	MCT4 MOUSE	P21812 mus muscu	533	335	24.4	701	2	Q9JJS9	Q9jjs9 rattus norv
461	340.5	24.8	274	1	TRY1_ANOGA	P35035 anopheles g	534	335	24.4	703	2	Q8CHN8	Q8chn8 rattus norv
462	340.5	24.8	446	1	FA7 RAT	Q8k3u6 rattus norv	535	334.5	24.3	247	2	Q70500	Q70500 rattus norv
463	340.5	24.8	624	2	Q9DAT3	Q9dat3 mus muscu	536	334.5	24.3	263	1	GRAX_MOUSE	O35205 mus muscu
464	340	24.7	273	2	Q9XSM1	Q9xsm1 ovis aries	537	334.5	24.3	275	2	Q7YS62	Q7ys62 equus cabal
465	340	24.7	280	2	Q8N171	Q8n171 homo sapien	538	334.5	24.3	537	2	Q9BYE1	Q9bye1 homo sapien
466	340	24.7	297	2	Q88781	Q88781 rattus ratt	539	334.5	24.3	581	2	Q9BYE2	Q9bye2 homo sapien
467	340	24.7	360	2	Q17489	Q17489 anopheles g	540	334	24.3	234	2	Q15096	Q15096 homo sapien
468	339.5	24.7	247	2	Q08732	Q08732 mesocricetu	541	334	24.3	264	2	Q8QGF6	Q8qgf6 xenopus lae
469	339.5	24.7	253	1	TRYB_DROER	P54625 drosophila	542	333.5	24.3	253	2	Q8MKZ1	Q8mkz1 drosophila

543	333.5	24.3	253	2	Q8SXZ4	O8sxz4 drosophila	616	328.5	23.9	365	2	Q7Q1D1	O7ql1d anopheles g
544	333.5	24.3	275	1	Q7PNF7	O7pnf7 anopheles g	617	328.5	23.9	524	2	Q7SXH8	O7sxh8 brachydanio
545	333.5	24.3	290	1	PR27_HUMAN	O9bqr3 homo sapien	618	328.5	23.9	615	2	Q6GNK4	O6gnk4 xenopus lae
546	333.5	24.3	824	2	Q61CC2	O6icc2 homo sapien	619	328.5	23.9	681	2	Q7ZT70	O7zt70 lampetra ja
547	333	24.2	245	1	CTRA_BOVIN	P00766 bos taurus	620	328.5	23.9	683	2	Q8MRHS	O8mrhs drosophila
548	333	24.2	256	2	Q9ROK0	O9rok0 mus musculus	621	328.5	23.9	786	1	STUB_DROME	O05319 drosophila
549	333	24.2	285	1	FA9_CAVPO	P16295 cavia porce	622	328.5	23.9	787	2	Q9VEY6	O9vey6 drosophila
550	333	24.2	320	2	Q7TOX2	O7tox2 xenopus lae	623	328.5	23.9	226	1	COGS_UCAPU	P00771 uca pugilal
551	333	24.2	355	2	Q7PEW0	O7pew0 anopheles g	624	328.5	23.9	328	2	Q6BEA2	O6bea2 rattus norv
552	333	24.2	360	2	Q7PEV7	O7pev7 anopheles g	625	328.5	23.9	452	1	PA9_CANFA	P19540 canis famil
553	332.5	24.2	247	2	Q35342	O35342 mesocricetu	626	328.5	23.9	767	2	Q9DGR2	O9dgr2 xenopus lae
554	332.5	24.2	254	2	Q8T637	O8t637 aedes aegypt	627	327.5	23.8	247	1	MCT1_MACFA	P56435 macaca fasc
555	332.5	24.2	260	2	Q8T4P6	O8t4p6 lepeophthei	628	327.5	23.8	263	2	Q9TY16	O9ty16 penaeus van
556	332.5	24.2	262	2	Q8T4P7	O8t4p7 lepeophthei	629	327.5	23.8	266	2	Q27761	O27761 penaeus van
557	332.5	24.2	263	2	Q7Z1D5	O7z1d5 lepeophthei	630	327.5	23.8	269	2	Q96QV5	O96qv5 homo sapien
558	332.5	24.2	264	2	Q7YSS9	O7yss9 lepeophthei	631	327.5	23.8	269	2	O6ISM5	O6ism5 homo sapien
559	332.5	24.2	490	1	TMS2_MOUSE	O9fjg8 mus musculus	632	327.5	23.8	269	2	Q6GN82	O6gn82 xenopus lae
560	332.5	24.2	638	1	KAL_RAT	P14272 rattus norv	633	327.5	23.8	259	1	DEF3_DERFA	F49275 dermatophag
561	332.5	24.2	810	1	PLMN_ERIEU	O29485 erinaceus e	634	327.5	23.8	263	2	Q7SYS4	O7sys4 xenopus lae
562	332.5	24.2	810	1	PLMN_MACMU	P12545 macaca mula	635	327.5	23.8	270	2	Q27824	O27824 uca pugilal
563	332	24.2	247	2	Q70T74	O70t74 equus cabal	636	327.5	23.8	466	2	Q6SA95	O6sa95 felis silve
564	332	24.2	251	2	Q7Q5W2	O7q5w2 anopheles g	637	327.5	23.8	600	2	Q7ZTR2	O7ztr2 xenopus lae
565	332	24.2	258	2	Q97399	O97399 phaedon coc	638	326.5	23.8	248	1	GRAC_MOUSE	P08882 mus musculus
566	332	24.2	266	2	Q92077	O92077 gadus morhu	639	326.5	23.8	263	2	Q6GNF7	O6gnf7 xenopus lae
567	332	24.2	277	2	Q8SQ44	O8sq44 sus scrofa	640	326.5	23.8	266	1	EL1_PIG	P00772 sus scrofa
568	332	24.2	355	2	Q9NFU1	O9nfu1 anopheles g	641	326.5	23.8	266	2	Q91X79	O91x79 mus musculus
569	331.5	24.1	250	2	Q8T4P4	O8t4p4 lepeophthei	642	326.5	23.8	369	2	Q7QKL1	O7qkl1 anopheles g
570	331.5	24.1	254	2	Q8MMK9	O8mmk9 aedes aegypt	643	326.5	23.8	490	2	Q7TN04	O7tn04 mus musculus
571	331.5	24.1	256	1	TRYA_DROME	P04814 drosophila	644	326.5	23.7	248	1	GRZ1_RAT	O06605 rattus norv
572	331.5	24.1	260	2	O8T4P5	O8t4p5 lepeophthei	645	326.5	23.7	271	1	CTR2_PENVA	P36178 penaeus van
573	331.5	24.1	263	2	Q9PWQ6	O9pwq6 gadus morhu	646	326.5	23.7	329	2	Q7PEV8	O7pev8 anopheles g
574	331.5	24.1	264	2	Q6GPY5	O6gpy5 xenopus lae	647	326.5	23.7	432	2	Q7QKL4	O7qkl4 anopheles g
575	331.5	24.1	275	1	TRY3_ANOGA	P35037 anopheles g	648	325.5	23.7	259	2	Q8IRE0	O8ire0 drosophila
576	331	24.1	263	1	CTRB_RAT	P07338 rattus norv	649	325.5	23.7	261	1	DER3_DERPT	P39675 dermatophag
577	331	24.1	622	1	THRB_HUMAN	P00734 homo sapien	650	325.5	23.7	268	2	O46151	O46151 pacifastacu
578	331	24.1	622	2	Q7Z7P3	O7z7p3 homo sapien	651	325.5	23.7	306	1	BSS4_MOUSE	O9er10 mus musculus
579	331	24.1	722	2	Q8AW90	O8aw90 lampetra ja	652	325.5	23.7	891	2	Q9VV38	O9vv38 drosophila
580	331	24.1	722	2	Q9PSZ5	O9ps25 lampetra ja	653	324.5	23.6	146	2	Q9DDE1	O9ddel brachydanio
581	330.5	24.1	247	1	MCT1_HUMAN	P23946 homo sapien	654	324.5	23.6	228	2	Q7Q153	O7q153 anopheles g
582	330.5	24.1	256	1	TRYA_DROER	P54624 drosophila	655	324.5	23.6	263	2	Q7PUB9	O7pub9 anopheles g
583	330.5	24.1	259	2	Q61SP9	O6isp9 homo sapien	656	324.5	23.6	275	1	TRYA_HUMAN	P15157 homo sapien
584	330.5	24.1	560	2	Q14520	O14520 homo sapien	657	324.5	23.6	391	2	Q9V3Z2	O9v3z2 drosophila
585	330.5	24.1	638	2	Q8ROP5	O8rop5 mus musculus	658	324.5	23.6	253	1	TRYB_DROME	P35004 drosophila
586	330	24.0	236	2	Q7SIG3	O7sig3 salmo salar	659	324.5	23.6	257	1	GRAM_HUMAN	P51124 homo sapien
587	330	24.0	253	2	Q9V5Y3	O9v5y3 drosophila	660	324.5	23.6	266	2	Q9W7Q0	O9w7q0 paralichthy
588	330	24.0	266	2	O81916	O8i916 blonnia trop	661	324.5	23.6	459	1	FA9_MOUSE	P16294 mus musculus
589	330	24.0	282	1	FA9_RAT	P16296 rattus norv	662	324.5	23.6	1019	1	ENTK_HUMAN	P98073 homo sapien
590	330	24.0	4548	1	APOA_HUMAN	P08519 homo sapien	663	323.5	23.5	277	2	Q80WM7	O80wm7 mus musculus
591	329.5	24.0	237	2	Q29464	O29464 bos taurus	664	323.5	23.5	299	2	Q9VS87	O9vs87 drosophila
592	329.5	24.0	248	2	O8T4P2	O8t4p2 lepeophthei	665	323.5	23.5	328	2	Q8BJR6	O8bjr6 mus musculus
593	329.5	24.0	253	1	TRYD_DROME	P42276 drosophila	666	323.5	23.5	466	1	FA7_HUMAN	P08709 homo sapien
594	329.5	24.0	262	2	Q7Z1D6	O7z1d6 lepeophthei	667	323.5	23.5	490	2	Q6P7D7	O6p7d7 rattus norv
595	329.5	24.0	266	2	Q8WR10	O8wr10 paralithode	668	323.5	23.5	608	2	Q9PTW7	O9ptw7 struthio ca
596	329.5	24.0	269	1	EL2B_HUMAN	P08218 homo sapien	669	323.5	23.5	875	1	NETR_HUMAN	P56730 homo sapien
597	329.5	24.0	320	2	Q7PEV6	O7pev6 anopheles g	670	323.5	23.5	281	2	O46137	O46137 lumbricus r
598	329.5	24.0	578	2	Q6Q017	O6q017 bos taurus	671	323.5	23.5	296	2	Q9VDV1	O9vdv1 drosophila
599	329.5	24.0	1420	1	APOA_MACMU	P14417 macaca mula	672	323.5	23.5	540	2	Q800Y7	O800y7 melesgris g
600	329	23.9	216	1	VSPB_LACMU	P84036 lachesis mu	673	323.5	23.5	653	2	Q8VCS4	O8vc4 mus musculus
601	329	23.9	284	2	O08643	O08643 mus musculus	674	323.5	23.5	653	2	Q8VCS4	O8vc4 mus musculus
602	329	23.9	279	2	Q99MS4	O99ms4 mus musculus	675	322.5	23.5	249	2	Q6QX62	O6qx62 lepeophthei
603	329	23.9	307	2	Q7TML0	O7tml0 mus musculus	676	322.5	23.5	258	2	Q9W5U8	O9wsu8 drosophila
604	329	23.9	572	2	Q8BIK6	O8bik6 mus musculus	677	322.5	23.5	324	1	TEST_MOUSE	O9jh17 mus musculus
605	329	23.9	575	2	Q7Q9W3	O7q9w3 anopheles g	678	322.5	23.5	336	2	Q80YD8	O80yd8 mus musculus
606	329	23.9	722	2	Q6NUF5	O6nuf5 xenopus lae	679	322.5	23.5	372	2	Q9Y1K6	O9y1k6 anopheles g
607	328.5	23.9	239	2	Q8T4P3	O8t4p3 lepeophthei	680	322.5	23.5	581	2	Q9XZM7	O9xzm7 strongyloce
608	328.5	23.9	245	1	CTRB_GADMO	P80646 gadus morhu	681	322.5	23.4	210	2	Q68DS2	O68ds2 homo sapien
609	328.5	23.9	253	1	TRYG_DROME	P42277 drosophila	682	322.5	23.4	699	1	CRAR_HUMAN	P48740 h complemen
610	328.5	23.9	260	1	MCT1_RAT	P09650 rattus norv	683	322.5	23.4	1303	2	Q6S884	O6s884 oikopleura
611	328.5	23.9	261	2	O8T4P1	O8t4p1 lepeophthei	684	321.5	23.4	263	2	O62562	O62562 penaeus van
612	328.5	23.9	275	2	Q86TW8	O86tm8 homo sapien	685	321.5	23.4	265	2	O7SYX8	O7syx8 xenopus lae
613	328.5	23.9	276	2	Q86UAS	O86uas homo sapien	686	321.5	23.4	286	2	Q9D936	O9d936 mus musculus
614	328.5	23.9	338	1	PLMN_HORSE	P80010 equus cabal	687	321.5	23.4	679	2	Q9A5P8	O9ap8 homo sapien
615	328.5	23.9	364	2	Q9NA59	O9nas9 anopheles g	688	321	23.4	226	1	DDN1_BOVIN	P80219 bos taurus

689	321	23.4	230	2	O61E13	O61E13 rattus norv	762	314	22.9	629	2	O6AZS7	O6azs7 xenopus lae
690	321	23.4	247	1	MCT2_MERUN	P50341 meriones un	763	314	22.9	855	1	ST14_HUMAN	Q9Y566 homo sapien
691	321	23.4	248	1	NKPI_RAT	P18291 rattus norv	764	313.5	22.8	261	1	EUM3_EURMA	O97370 euroglyphus
692	321	23.4	269	1	TRYM_CANPA	P19236 canis famli	765	313.5	22.8	321	1	O80Y38	O80y38 mus musculus
693	321	23.4	411	2	Q9VUF0	Q9vuf0 drosophila	766	313.5	22.8	326	2	Q9D9M0	Q9d9m0 mus musculus
694	321	23.4	655	1	HGFA_HUMAN	Q04756 homo sapien	767	313.5	22.8	364	2	Q917V4	Q917v4 drosophila
695	320.5	23.3	247	1	GRAB_MOUSE	P04187 mus musculus	768	313.5	22.8	425	2	O804X7	O804x7 gallus gall
696	320.5	23.3	312	2	Q7M755	Q7m755 mus musculus	769	313	22.8	241	2	Q917L2	Q917l2 drosophila
697	320	23.3	249	2	Q9W7Q1	Q9w7q1 paralichthy	770	313	22.8	336	2	Q8CIR9	Q8c19 mus musculus
698	320	23.3	489	2	Q7Q432	Q7q432 anopheles g	771	313	22.8	420	2	Q90504	Q90504 eptaretus
699	320	23.3	536	2	Q7PX72	Q7px72 anopheles g	772	313	22.8	613	2	Q03711	Q03711 xenopus lae
700	319.5	23.3	265	2	O6GNG0	O6gng0 xenopus lae	773	313	22.8	697	2	O8CG43	O8cg43 rattus norv
701	319.5	23.3	559	2	O6P7U0	O6p7u0 mus musculus	774	313	22.8	733	2	Q920S0	Q920s0 mus musculus
702	319.5	23.3	607	2	O6DRJ5	O6drj5 xenopus lae	775	313	22.8	733	2	Q8CD27	Q8cd27 mus musculus
703	319	23.2	241	2	Q7PPE7	Q7ppe7 anopheles g	776	313	22.8	855	2	Q90U17	Q90u17 rattus norv
704	319	23.2	264	2	Q81PF7	Q81pf7 drosophila	777	312.5	22.7	241	2	O81YP2	O81yp2 homo sapien
705	319	23.2	270	2	O641D1	O641d1 anthonomus	778	312.5	22.7	271	2	O819R6	O819r6 culex pipie
706	319	23.2	320	2	O8CIR7	O8cir7 rattus norv	779	312.5	22.7	274	1	TRV5_ANOGA	P35039 anopheles g
707	319	23.2	461	2	Q95ND6	Q95nd6 pan troglod	780	312.5	22.7	300	2	O96EF3	O96ef3 homo sapien
708	319	23.2	1034	1	ENTK_PIG	P98074 sus scrofa	781	312.5	22.7	390	2	Q9Y157	Q9y157 drosophila
709	318.5	23.2	343	1	PLMN_SHEEP	P81286 ovis aries	782	312.5	22.7	615	1	FA12_HUMAN	P00748 homo sapien
710	318.5	23.2	418	2	O61E15	O61e15 rattus norv	783	312.5	22.7	680	2	O868H5	O868h5 branchiosto
711	318.5	23.2	490	2	Q920K3	Q920k3 rattus norv	784	312.5	22.7	1234	2	Q7PIQ7	Q7piq7 anopheles g
712	318	23.1	232	2	Q94508	Q94508 dermatophag	785	312.5	22.7	1322	2	Q7PNR7	Q7pnr7 anopheles g
713	318	23.1	258	2	Q7YRZ7	Q7yrz7 bos taurus	786	312.5	22.7	1322	2	Q9NJS5	Q9njrs anopheles g
714	318	23.1	261	2	O962G7	O962g7 culex pipie	787	312	22.7	395	2	O8CIP7	O8cip7 rattus norv
715	318	23.1	265	2	O18488	O18488 penaeus van	788	312	22.7	374	2	O81862	O81862 dermacentor
716	318	23.1	271	1	FA9_PIG	P16293 sus scrofa	789	312	22.7	597	2	O35727	O35727 mus musculus
717	318	23.1	274	1	FA9_SHEEP	P16291 ovis aries	790	312	22.7	597	2	O8PER0	O8per0 mus musculus
718	318	23.1	295	2	O69E28	O69e28 homo sapien	791	312	22.7	609	2	Q80YC5	Q80yc5 mus musculus
719	318	23.1	618	1	THRB_MOUSE	P19221 mus musculus	792	311.5	22.7	255	2	O25227	O25227 lucilia cup
720	317.5	23.1	245	1	CTRB_BOVIN	P00767 bos taurus	793	311.5	22.7	255	2	O7TNI0	O7tni0 mus musculus
721	317.5	23.1	246	1	GRAH_HUMAN	P20718 homo sapien	794	311.5	22.7	293	2	O23528	O23528 caenorhabdi
722	317.5	23.1	248	2	O9XYX9	O9xyx9 rhizopertha	795	311.5	22.7	566	1	TPA_BOVIN	Q28198 bos taurus
723	317.5	23.1	256	1	TRYE_DROER	P54627 drosophila	796	311.5	22.7	645	2	Q7PWE4	O08762 mus musculus
724	317.5	23.1	374	2	Q9VUG2	Q9vug2 drosophila	797	311.5	22.7	761	1	NETR_MOUSE	Q9nat0 anopheles g
725	317.5	23.1	559	1	TPA_MOUSE	P11214 mus musculus	798	311.5	22.7	1322	2	Q9NAT0	O9nat0 anopheles g
726	317.5	23.1	604	1	Q8JIS1	Q8j1s1 rattus norv	799	311	22.6	249	2	O61E11	O61e11 rattus norv
727	317.5	23.1	617	2	O8JIS1	O8j1s1 triakis scy	800	311	22.6	250	2	Q9V514	Q9v514 drosophila
728	317	23.1	248	2	O63636	O63636 rattus norv	801	311	22.6	261	1	CATG_MOUSE	P28293 mus musculus
729	317	23.1	624	2	Q95NE7	Q95ne7 oryctolagus	802	311	22.6	431	1	ACRO_RABIT	P48038 oryctolagus
730	316.5	23.0	246	1	MCT1_MOUSE	P11034 mus musculus	803	311	22.6	433	1	UROK_BOVIN	Q05589 bos taurus
731	316.5	23.0	441	2	O81917	O81917 manduca sex	804	311	22.6	1035	1	ENTK_BOVIN	P98072 bos taurus
732	316.5	23.0	607	2	Q91001	Q91001 gallus gall	805	311	22.6	1042	1	CORI_HUMAN	O9Y5G5 homo sapien
733	316	23.0	246	2	O9XV46	O9xv46 ctenocephal	806	310.5	22.6	247	1	MCT2_RAT	P00770 rattus norv
734	316	23.0	259	2	O69E27	O69e27 homo sapien	807	310.5	22.6	259	2	Q7PFI7	Q7pfi7 anopheles g
735	316	23.0	263	2	O02570	O02570 culex quinq	808	310.5	22.6	371	2	O8MRV3	Q8mry3 drosophila
736	316	23.0	289	2	Q9CQ52	Q9cq52 m mus muscu	809	310.5	22.6	473	2	O7PV63	Q7pv63 anopheles g
737	316	23.0	289	2	Q9D7T9	Q9d7t9 mus musculus	810	310.5	22.6	559	1	TPA_RAT	P19637 rattus norv
738	315.5	23.0	254	1	TRY3_AEDAE	P29786 aedes aegyp	811	310.5	22.6	1374	2	Q9VSU0	Q9vsu0 drosophila
739	315.5	23.0	264	2	O62561	O62561 penaeus van	812	310.5	22.6	1449	2	O9U112	O9u112 drosophila
740	315.5	23.0	265	2	O66KR6	O66kr6 xenopus lae	813	310.5	22.6	1450	2	O8IQB8	O8iqb8 drosophila
741	315.5	23.0	266	1	ELL_RAT	P00773 rattus norv	814	310.5	22.6	1462	2	Q9U113	Q9u113 drosophila
742	315.5	23.0	314	2	Q9VR15	Q9vr15 drosophila	815	310.5	22.6	2382	2	O9B119	O9b119 drosophila
743	315.5	23.0	374	2	Q7QCS5	Q7qcs5 anopheles g	816	310.5	22.6	2409	2	Q960G6	Q960g6 drosophila
744	315.5	23.0	392	1	EAST_DROME	P13582 drosophila	817	310.5	22.6	2786	2	Q9VSU2	Q9vsu2 drosophila
745	315.5	23.0	453	2	O812A6	O812a6 mus musculus	818	310	22.6	275	1	FA9_RABIT	P16292 oryctolagus
746	315.5	23.0	492	1	FA10_BOVIN	P00743 bos taurus	819	310	22.6	327	1	Q7Q530	Q7q530 anopheles g
747	315	22.9	248	2	O63224	O63224 rattus norv	820	310	22.6	483	2	O8T8X4	O8t8x4 drosophila
748	315	22.9	280	2	O66NX6	O66nx6 canis famli	821	310	22.6	483	2	O9VK10	Q9vk10 drosophila
749	315	22.9	323	2	Q96QG4	Q96qg4 homo sapien	822	310	22.6	1111	2	O8QYN4	O8qyn4 rattus norv
750	315	22.9	617	1	THRB_RAT	P18292 rattus norv	823	309.5	22.5	246	2	O9EPR0	Q9epro mus musculus
751	315	22.9	686	1	MAS2_HUMAN	O00187 homo sapien	824	309.5	22.5	255	2	O9Y7A9	Q9y7a9 metarhizium
752	314.5	22.9	256	1	TRYE_DROME	P35005 drosophila	825	309.5	22.5	265	2	Q9VVT3	Q9vvt3 drosophila
753	314.5	22.9	261	2	O6IDF4	O6idf4 drosophila	826	309.5	22.5	284	2	Q7Q493	Q7q493 anopheles g
754	314.5	22.9	283	1	O6UWY2	O6uwy2 homo sapien	827	309.5	22.5	482	1	FA10_RAT	Q63207 rattus norv
755	314.5	22.9	453	1	TMS3_MOUSE	O8kt0 mus musculus	828	309.5	22.5	868	2	Q9Y1V3	Q9y1v3 polyandroca
756	314.5	22.9	609	2	Q7M761	Q7m761 mus musculus	829	309	22.5	285	2	O8CG42	Q8cg42 rattus norv
757	314.5	22.9	680	2	O868H7	O868h7 branchiosto	830	309	22.5	404	2	O7QKL2	Q7qkl2 anopheles g
758	314	22.9	275	1	TRY4_ANOGA	P35038 anopheles g	831	308.5	22.5	240	2	O6IE06	Q6ie06 rattus norv
759	314	22.9	280	2	Q7Q494	Q7q494 anopheles g	832	308.5	22.5	246	1	MCT1_MOUSE	O35164 mus musculus
760	314	22.9	280	2	O66NX5	O66nx5 canis famli	833	308.5	22.5	260	2	O6VPÜ6	Q6vpü6 sarcopes s
761	314	22.9	422	2	Q8WVC1	Q8wvc1 homo sapien	834	308	22.4	125	2	Q804G0	Q804g0 sphoeroides

835	308	22.4	300	2	Q819P4	Q819P4 aurelia aur	908	302	22.0	269	2	Q7PW17	Q7pw17 anopheles g
836	308	22.4	317	1	BSS4_HUMAN	Q9gzr4 homo sapien	909	302	22.0	321	2	Q6MZL2	Q6mzl2 homo sapien
837	308	22.4	334	2	Q6UXE0	Q6uxe0 homo sapien	910	302	22.0	394	1	URTG_DESRO	P49150 desmodus ro
838	308	22.4	335	2	Q86PB3	Q86pb3 drosophila	911	302	22.0	477	1	URBT_DESRO	P15638 desmodus ro
839	308	22.4	337	2	Q9VB68	Q9vb68 drosophila	912	301.5	21.9	241	2	Q8BW11	Q8bw11 m mus muscu
840	308	22.4	408	2	Q8MR95	Q8mr95 drosophila	913	301.5	21.9	394	2	P91817	P91817 tachypleus
841	308	22.4	698	2	Q6GPF9	Q6gpf9 xenopus lae	914	301.5	21.9	505	2	Q7QCv2	Q7qcv2 anopheles g
842	307.5	22.4	255	2	Q7PFF16	Q7pff16 anopheles g	915	301	21.9	255	1	CATG_HUMAN	P08311 homo sapien
843	307.5	22.4	471	2	Q804X6	Q804x6 gallus gall	916	301	21.9	255	2	Q34289	Q34289 salvelinus
844	307.5	22.4	676	2	Q6DUJ6	Q6duj6 cyprinus ca	917	301	21.9	268	2	Q17030	Q17030 anopheles g
845	307	22.3	135	2	Q62284	Q62284 mus musculus	918	301	21.9	279	2	Q7PX39	Q7px39 anopheles g
846	307	22.3	250	2	Q17036	Q17036 anopheles g	919	301	21.9	279	2	Q7TNX3	Q7tnx3 mus musculus
847	307	22.3	259	1	CTRI_ANOGA	Q27289 anopheles g	920	301	21.9	283	2	Q9SV22	Q9sv22 lumbricus b
848	307	22.3	318	2	Q7Q9W4	Q7q9w4 anopheles g	921	301	21.9	417	2	Q8VHK8	Q8vhk8 mus musculus
849	307	22.3	417	1	HEPS_HUMAN	P05981 homo sapien	922	301	21.9	417	2	Q8VDV1	Q8vdl1 mus musculus
850	307	22.3	726	2	Q7QBPA	Q7qbp4 anopheles g	923	301	21.9	431	1	URTB_DESRO	P98121 desmodus ro
851	306.5	22.3	308	2	Q9W454	Q9w454 drosophila	924	301	21.9	728	2	Q96RS4	Q96rs4 homo sapien
852	306.5	22.3	365	2	Q7QGL1	Q7qgl1 anopheles g	925	300.5	21.9	239	2	Q772H1	Q772h1 xenopus lae
853	306.5	22.3	375	1	PCE_TACTR	P21902 tachypleus	926	300.5	21.9	276	2	P91894	P91894 arenicola m
854	306.5	22.3	418	2	Q8S2K2	Q8s2k2 drosophila	927	300.5	21.9	278	2	Q68FN6	Q68fn6 brachydanio
855	306.5	22.3	468	2	Q9UUG3	Q9uug3 pacifastacu	928	300.5	21.9	386	2	Q81924	Q81924 bombyx mori
856	306	22.3	162	2	Q6UBM2	Q6ubm2 homo sapien	929	300.5	21.9	424	2	Q9VA88	Q9va88 drosophila
857	306	22.3	247	2	Q8N1D2	Q8nid2 homo sapien	930	300.5	21.9	433	2	Q8MHY7	Q8mhy7 oryctolagus
858	306	22.3	266	2	Q6AZC0	Q6azc0 brachydanio	931	300.5	21.9	433	2	Q8MIL0	Q8mil0 oryctolagus
859	306	22.3	362	2	Q9W453	Q9w453 drosophila	932	300.5	21.9	442	1	UROK_PIG	P04185 sus scrofa
860	306	22.3	685	2	Q91WP0	Q91wp0 mus musculus	933	300.5	21.9	562	2	Q8SQ23	Q8sq23 sus scrofa
861	305.5	22.2	228	2	Q9XY49	Q9xy49 ctenocephal	934	300	21.8	245	1	GILX_HELHO	P43685 heloderma h
862	305.5	22.2	246	2	Q91VB1	Q91vb1 mus musculus	935	300	21.8	270	2	Q8WR11	Q8wr11 paralichode
863	305.5	22.2	256	1	HYPA_HYPLI	P15587 hypoderma l	936	300	21.8	291	2	Q81Q89	Q81q89 drosophila
864	305.5	22.2	274	2	Q6GNF0	Q6gnf0 xenopus lae	937	300	21.8	417	2	Q8VHJ4	Q8vhj4 rattus norv
865	305.5	22.2	383	2	Q77102	Q77102 manduca sex	938	300	21.8	698	2	Q9PU71	Q9pu71 xenopus lae
866	305.5	22.2	418	2	Q9VA87	Q9va87 drosophila	939	299.5	21.8	241	2	Q63637	Q63637 rattus norv
867	305.5	22.2	441	2	Q804X2	Q804x2 fugu rubrip	940	299.5	21.8	246	1	MCTX_MOUSE	Q00356 mus musculus
868	305	22.2	247	1	GRAB_HUMAN	P10144 h granzyme	941	299.5	21.8	254	2	Q6DBS8	Q6dbse8 brachydanio
869	305	22.2	281	2	Q67BC3	Q67bc3 homo sapien	942	299.5	21.8	257	2	Q19023	Q19023 macaca mula
870	305	22.2	307	2	Q641D2	Q641d2 anthonomus	943	299.5	21.8	258	1	CTR2_ANOGA	Q17025 anopheles g
871	305	22.2	391	2	Q7PXPJ5	Q7pxj5 anopheles g	944	299.5	21.8	272	2	Q7Q9W5	Q7q9w5 anopheles g
872	305	22.2	395	2	Q9BZW1	Q9bzw1 homo sapien	945	299.5	21.8	282	2	Q7PT16	Q7pt16 anopheles g
873	305	22.2	532	2	Q7PXP73	Q7px73 anopheles g	946	299.5	21.8	325	2	O15944	O15944 sarcophaga
874	304.5	22.2	258	2	Q9XY53	Q9xy53 ctenocephal	947	299.5	21.8	372	2	Q9W2C8	Q9w2c8 drosophila
875	304.5	22.2	271	2	Q7Q820	Q7q820 anopheles g	948	299.5	21.8	430	2	Q6RUJ3	Q6ruj3 trichinella
876	304.5	22.2	384	2	Q9XY63	Q9xy63 ctenocephal	949	299.5	21.8	436	1	ACRO_MOUSE	P23578 mus musculus
877	304.5	22.2	492	1	TMS2_HUMAN	O15393 homo sapien	950	299.5	21.8	465	2	Q9BUL7	Q9bjl7 trichinella
878	304.5	22.2	492	2	Q6ET73	Q6et73 homo sapien	951	299.5	21.8	615	2	Q81ZZ5	Q81zz5 homo sapien
879	304	22.1	268	1	CLCR_HUMAN	Q99895 homo sapien	952	299.5	21.8	974	2	Q90WD8	Q90wd8 bufo japoni
880	304	22.1	272	2	Q9XYV6	Q9xyv6 rhizopertha	953	299.5	21.8	1069	1	ENTK_MOUSE	P97435 mus musculus
881	304	22.1	375	2	Q817W8	Q817w8 dermacentor	954	299	21.8	256	2	Q6VLQ1	Q6vlq1 verticilliu
882	304	22.1	393	2	Q6RX66	Q6rx66 armigeres s	955	299	21.8	437	1	ACRO_RAT	P29293 rattus norv
883	304	22.1	400	2	Q9VCJ8	Q9vcj8 drosophila	956	298.5	21.7	235	2	Q91004	Q91004 gekko gekko
884	304	22.1	423	2	Q8BM10	Q8bm10 mus musculus	957	298.5	21.7	248	2	Q9VQ98	Q9vq98 drosophila
885	304	22.1	543	2	Q9BU99	Q9bu99 homo sapien	958	298.5	21.7	249	1	MCT1_CANFA	P21842 canis famli
886	304	22.1	562	1	TPA_HUMAN	P00750 homo sapien	959	298.5	21.7	350	2	Q7OKY0	Q7oky0 anopheles g
887	304	22.1	589	2	Q6PJAS	Q6pjas homo sapien	960	298.5	21.7	407	1	FA7_BOVIN	P22457 bos taurus
888	304	22.1	685	2	Q92338	Q92338 mus musculus	961	298.5	21.7	433	2	Q8T3A2	Q8t3a2 ciona intes
889	304	22.1	1379	2	Q9V4N6	Q9v4n6 drosophila	962	298.5	21.7	733	2	Q9VTX9	Q9vtx9 drosophila
890	304	22.1	1397	2	Q7KQO9	Q7kqg9 drosophila	963	298	21.7	235	2	Q28731	Q28731 oryctolagus
891	303.5	22.1	240	1	MCT5_MOUSE	P15119 mus musculus	964	298	21.7	255	2	O18435	O18435 helicoverpa
892	303.5	22.1	244	1	MCT2_MOUSE	Q7syg8 xenopus lae	965	298	21.7	268	2	Q8T4T4	Q8t4t4 aedes aegyp
893	303.5	22.1	246	1	MCT4_RAT	P97592 rattus norv	966	298	21.7	348	2	Q86WS5	Q86ws5 homo sapien
894	303.5	22.1	278	2	Q7Q492	Q7q492 anopheles g	967	297.5	21.7	254	2	Q76520	Q76520 stomoxys ca
895	303.5	22.1	309	2	Q72083	Q72083 tachypleus	968	297.5	21.7	256	2	Q6MJY6	Q6mly6 bdellovibri
896	303.5	22.1	603	1	CFAI_MOUSE	Q61129 mus musculus	969	297.5	21.7	269	2	Q6AZF9	Q6azf9 xenopus lae
897	303.5	22.1	761	2	Q99JC8	Q99jc8 rattus norv	970	297.5	21.7	277	2	Q81Q10	Q81q10 drosophila
898	303	22.1	246	1	MCT2_SHEEP	P79204 ovis aries	971	297.5	21.7	293	2	Q7Q8F9	Q7q8f9 anopheles g
899	303	22.1	259	2	Q6JPF5	Q6jpf5 neodiprion	972	297.5	21.7	408	2	Q9VM19	Q9vm19 drosophila
900	302.5	22.0	119	2	Q9NR68	Q9nr68 homo sapien	973	297.5	21.7	435	1	SNAK_DROME	P05049 drosophila
901	302.5	22.0	223	2	Q9VB44	P35044 drosophila	974	297.5	21.7	472	2	Q7Q182	Q7q182 anopheles g
902	302.5	22.0	273	1	TRY6_ANOGA	P35040 anopheles g	975	297.5	21.7	486	2	Q7EX74	Q7ex74 anopheles g
903	302.5	22.0	1004	2	P79953	P79953 xenopus lae	976	297.5	21.7	519	2	Q8T3A3	Q8t3a3 ciona intes
904	302.5	22.0	1113	1	CORI_MOUSE	Q9z319 mus musculus	977	297.5	21.7	616	2	Q97507	Q97507 sus scrofa
905	302	22.0	247	2	Q6TJ76	Q6tj76 eisenia foe	978	297	21.6	237	1	TRYP_ASTFL	P00765 astacus flu
906	302	22.0	255	1	TRY4_LUCCU	P35044 lucilia cup	979	297	21.6	247	1	MCT5_MOUSE	P21844 mus musculus
907	302	22.0	268	2	Q9W7Q2	Q9w7q2 paralichthy	980	297	21.6	256	2	Q9XY51	Q9xy51 ctenocephal

981	297	21.6	268	2	Q9BIG0	Q9big0 aedes aegyp	1054	291.5	21.2	270	2	Q7Q5A6	Q7q5a6 anopheles g
982	297	21.6	284	2	Q8IRX5	Q8irx5 drosophila	1055	291	21.2	239	2	Q6LCU4	Q6lcu4 lumbricus r
983	297	21.6	352	2	Q6UMB4	Q6umb4 homo sapien	1056	291	21.2	271	2	Q542I3	Q542i3 streptomyce
984	297	21.6	369	2	Q6AXZ6	Q6axz6 rattus norv	1057	291	21.2	436	1	HEFS_MOUSE	Q35453 mus musculus
985	297	21.6	454	1	TMS3_HUMAN	P57727 desmodius ro	1058	291	21.2	678	2	Q7QJUS8	Q7qj8 rattus norv
986	297	21.6	477	1	URT1_DESRO	P98119 desmodius ro	1059	290.5	21.1	483	2	Q7PKJ7	Q7pkj7 anopheles g
987	297	21.6	248	1	GRAF_MOUSE	P08883 mus musculus	1060	290.5	21.1	681	2	Q7Q554	Q7q554 anopheles g
988	296.5	21.6	248	1	EL3B_HUMAN	P08861 homo sapien	1061	290	21.1	149	2	Q6DTY8	Q6dty8 hypophthalm
989	296.5	21.6	272	2	Q9V5X6	Q9v5x6 drosophila	1062	290	21.1	256	1	HYPB_HYPLI	P35888 hypoderma l
990	296.5	21.6	273	2	Q7JYN3	Q7jyn3 drosophila	1063	290	21.1	257	2	Q8I927	Q8i927 hyphantria
991	296.5	21.6	581	2	Q96O15	Q96o15 drosophila	1064	290	21.1	390	2	Q8I927	Q8i927 hyphantria
992	296.5	21.6	1047	2	Q9VZ82	Q9vz82 drosophila	1065	289.5	21.1	246	2	Q9BLI7	Q9bli7 lumbricus r
993	296	21.5	265	2	Q74696	Q74696 phaeosphaer	1066	289.5	21.1	248	1	GRAG_MOUSE	P13366 mus musculus
994	296	21.5	279	2	Q9Q274	Q9q274 rattus norv	1067	289.5	21.1	257	2	Q6RS60	Q6rs60 ostrinia nu
995	296	21.5	281	2	Q76898	Q76898 drosophila	1068	289.5	21.1	317	2	Q8K4I7	Q8k4i7 mus musculus
996	296	21.5	314	2	Q6RUT2	Q6rut2 mus musculus	1069	289	21.0	260	2	Q7RTY3	Q7rty3 homo sapien
997	296	21.5	318	2	Q8OUR4	Q8our4 mus musculus	1070	289	21.0	378	2	Q7QHS0	Q7qhs0 anopheles g
998	295.5	21.5	239	2	Q9GME0	Q9gme0 ornithorhyn	1071	289	21.0	339	2	Q9QX91	Q9qx91 rattus norv
999	295.5	21.5	239	2	Q9I218	Q9i218 oncorhynch	1072	289	21.0	366	2	Q9QX85	Q9qx85 rattus norv
1000	295.5	21.5	270	2	Q9VRS4	Q9vrs4 drosophila	1073	289	21.0	376	1	FAI10_TROCA	P81428 tropidochis
1001	295.5	21.5	433	1	UROK_MOUSE	P06869 mus musculus	1074	289	21.0	441	2	Q9XXV0	Q9xxv0 bombyx mori
1002	295.5	21.5	449	2	Q9VDU8	Q9vdu8 drosophila	1075	289	21.0	541	2	Q9QX90	Q9qx90 rattus norv
1003	295.5	21.5	453	2	Q6ZMC3	Q6zmc3 homo sapien	1076	289	21.0	583	1	CPAI_HUMAN	P05156 homo sapien
1004	295	21.5	260	2	Q9V6P6	Q9v6p6 drosophila	1077	289	21.0	623	2	Q9JUP3	Q9jup3 rattus norv
1005	295	21.5	267	2	Q6DCW4	Q6dcw4 brachydanio	1078	289	21.0	643	2	Q9QX84	Q9qx84 rattus norv
1006	295	21.5	268	2	Q8T4T5	Q8t4t5 aedes aegyp	1079	288.5	21.0	255	2	Q9XY62	Q9xy62 ctenocephal
1007	295	21.5	269	2	Q95KW7	Q95kw7 bos taurus	1080	288.5	21.0	264	2	Q7Q290	Q7q290 anopheles g
1008	295	21.5	358	2	Q45029	Q45029 drosophila	1081	288.5	21.0	315	2	Q8IRR3	Q8irr3 drosophila
1009	295	21.5	553	2	Q6P7I9	Q6p7i9 xenopus lae	1082	288.5	21.0	317	2	Q8K4D1	Q8k4d1 mus musculus
1010	294.5	21.4	244	2	Q8I6N3	Q8i6n3 eisenia foe	1083	288.5	21.0	438	2	Q6ZWK6	Q6zwk6 homo sapien
1011	294.5	21.4	575	2	Q8IRB8	Q8irb8 drosophila	1084	288.5	21.0	442	2	Q8O4X1	Q8o4x1 fugu rubrip
1012	294	21.4	247	2	Q6IE57	Q6ie57 rattus norv	1085	288.5	21.0	1047	2	Q24019	Q24019 drosophila
1013	294	21.4	259	2	Q9XY61	Q9xy61 ctenocephal	1086	288	21.0	257	2	Q9NB49	Q9nb49 aedes aegyp
1014	294	21.4	265	2	Q9VHF8	Q9vhf8 drosophila	1087	288	21.0	261	2	Q8IRE1	Q8ire1 drosophila
1015	294	21.4	271	2	Q9GTFK2	Q9gtfk2 culex quinq	1088	288	21.0	405	2	Q8NMZ7	Q8nmz7 anopheles g
1016	294	21.4	283	2	Q25394	Q25394 lumbricus r	1089	288	21.0	405	2	Q7PGY0	Q7pgy0 anopheles g
1017	294	21.4	283	2	Q8ITU7	Q8itu7 lumbricus r	1090	288	21.0	421	2	Q6O491	Q6o491 cavia porce
1018	294	21.4	293	2	Q7Z5A4	Q7z5a4 homo sapien	1091	288	21.0	730	2	Q6O1Q8	Q6o1q8 gallus gall
1019	294	21.4	303	2	Q76900	Q76900 drosophila	1092	287.5	20.9	234	2	Q9O244	Q9o244 acipenser t
1020	293.5	21.4	246	2	Q6IE10	Q6ie10 rattus norv	1093	287.5	20.9	244	2	Q6T375	Q6t375 eisenia foe
1021	293.5	21.4	256	2	Q9XY11	Q9xy11 rhyzopertha	1094	287.5	20.9	249	2	Q7KRD0	Q7krd0 drosophila
1022	293.5	21.4	257	2	Q7Z0G1	Q7z0g1 phlebotomus	1095	287.5	20.9	472	2	Q6IGB2	Q6igb2 drosophila
1023	293.5	21.4	302	2	Q8SYZ7	Q8syz7 drosophila	1096	287.5	20.9	603	1	FAI2_CAVPO	Q49562 cavia porce
1024	293.5	21.4	302	2	Q9W586	Q9w586 drosophila	1097	287.5	20.9	845	2	Q632Q6	Q632q6 xenopus lae
1025	293.5	21.4	431	1	UROK_HUMAN	P00749 homo sapien	1098	287	20.9	204	2	Q6S9W8	Q6s9w8 homo sapien
1026	293.5	21.4	845	2	Q6GR54	Q6gr54 xenopus lae	1099	287	20.9	244	2	Q6LAM0	Q6lam0 homo sapien
1027	293	21.3	246	2	Q9R2C8	Q9r2c8 rattus norv	1100	287	20.9	256	2	Q25081	Q25081 hypoderma l
1028	293	21.3	247	1	MCT3_RAT	P50339 rattus norv	1101	287	20.9	268	2	Q8T4T3	Q8t4t3 aedes aegyp
1029	293	21.3	265	1	SER1_DROME	P17205 drosophila	1102	287	20.9	273	2	Q9VEM5	Q9vem5 drosophila
1030	293	21.3	268	2	Q16900	Q16900 aedes aegyp	1103	287	20.9	416	2	Q86T26	Q86t26 homo sapien
1031	293	21.3	268	2	Q8NOR8	Q8nor8 aedes aegyp	1104	287	20.9	422	1	DES1_HUMAN	Q9ul52 homo sapien
1032	293	21.3	277	2	Q9VPN8	Q9vpn8 drosophila	1105	287	20.9	423	2	Q6UW31	Q6uw31 homo sapien
1033	293	21.3	278	2	Q8MQ02	Q8mq02 drosophila	1106	287	20.9	481	1	FAI10_MOUSE	Q88947 mus musculus
1034	293	21.3	301	2	Q7Q6U2	Q7q6u2 anopheles g	1107	287	20.9	581	2	Q8I925	Q8i925 hyphantria
1035	293	21.3	427	2	Q6Y2X4	Q6y2x4 manduca sex	1108	286.5	20.9	218	1	CTR2_VESCR	P00769 vespa crabr
1036	293	21.3	433	1	UROK_PAPCY	P16227 papio cynoc	1109	286.5	20.9	220	2	Q7QM61	Q7qm61 anopheles g
1037	293	21.3	777	2	Q8CAN9	Q8can9 mus musculus	1110	286.5	20.9	376	2	Q7PTP7	Q7ptp7 anopheles g
1038	293	21.3	855	1	ST14_MOUSE	P56677 mus musculus	1111	286.5	20.9	425	2	Q7EZ85	Q7ez85 anopheles g
1039	292.5	21.3	335	2	Q90387	Q90387 cynops pyrr	1112	286	20.8	235	2	Q6XGZ4	Q6xgz4 homo sapien
1040	292.5	21.3	336	2	Q9Z1H1	Q9z1h1 mus musculus	1113	286	20.8	254	1	CTRL_HALRU	P35003 haliotis ru
1041	292.5	21.3	390	2	Q8MP08	Q8mp08 bombyx mori	1114	286	20.8	272	2	Q7Q483	Q7q483 anopheles g
1042	292.5	21.3	459	2	Q9GMD9	Q9gmd9 ornithorhyn	1115	286	20.8	416	2	Q8BZ13	Q8bz13 mus musculus
1043	292	21.3	267	2	Q8T639	Q8t639 aedes aegyp	1116	286	20.8	416	2	Q8BZ30	Q8bz30 mus musculus
1044	292	21.3	268	1	CLCR_RAT	P55091 rattus norv	1117	286	20.8	443	2	Q8JHC9	Q8jhc9 brachydanio
1045	292	21.3	270	2	Q8T4A8	Q8t4a8 drosophila	1118	286	20.8	667	2	Q9BJM1	Q9bjm1 trichinella
1046	292	21.3	276	2	Q97398	Q97398 phaeton coc	1119	285.5	20.8	175	2	Q6PLJ9	Q6plj9 squilla ora
1047	292	21.3	332	2	Q8SYS8	Q8sys8 drosophila	1120	285.5	20.8	248	1	MCT8_RAT	P97594 rattus norv
1048	292	21.3	413	2	Q8T9T2	Q8t9t2 aedes aegyp	1121	285.5	20.8	270	1	EL3A_HUMAN	P09093 homo sapien
1049	292	21.3	475	2	Q8O4W9	Q8o4w9 fugu rubrip	1122	285.5	20.8	270	2	Q96QI8	Q96ql8 homo sapien
1050	292	21.3	688	2	Q868H6	Q868h6 branchiosto	1123	285.5	20.8	270	2	Q91039	Q91039 gadus morhu
1051	291.5	21.2	216	1	CTR2_VESOR	P00768 vespa orien	1124	285.5	20.8	289	2	Q8MR67	Q8mr67 drosophila
1052	291.5	21.2	238	2	Q9Z1D3	Q9z1d3 rattus norv	1125	285.5	20.8	290	2	Q9VRT2	Q9vrt2 drosophila
1053	291.5	21.2	255	2	Q9NBC9	Q9nbc9 glossina mo	1126	285	20.7	470	2	Q8T3A1	Q8t3a1 ciona intes



1127	284.5	20.7	172	2	Q6T776	Q6t776 homo sapien	1200	277	20.2	273	2	Q9VKA8	Q9vka8 drosophila
1128	284.5	20.7	245	2	Q6DKQ3	Q6dkq3 eisenia foe	1201	277	20.2	398	2	Q8MKP4	Q8mkp4 drosophila
1129	284.5	20.7	253	1	CAC3 BOVIN	P05805 bos taurus	1202	277	20.2	1629	2	Q9V513	Q9v513 drosophila
1130	284.5	20.7	564	2	Q7RTZ1	Q7rtz1 homo sapien	1203	277	20.2	1674	2	Q8SV35	Q8sv35 drosophila
1131	284	20.7	235	2	Q6B4R4	Q6b4r4 bos taurus	1204	276.5	20.1	257	2	Q9T099	Q9t099 anopheles d
1132	284	20.7	243	2	Q01309	Q01309 botryllus s	1205	276.5	20.1	262	2	Q9VSJ2	Q9vsj2 drosophila
1133	284	20.7	257	2	Q86PL8	Q86pl8 aedes aegypt	1206	276	20.1	254	1	PRN3 MOUSE	Q61096 mus musculus
1134	283.5	20.6	268	2	Q9XY56	Q9xy56 stenoccephal	1207	276	20.1	257	2	Q818E4	Q818e4 ochlerotatu
1135	283.5	20.6	707	2	Q8QGV0	Q8qgv0 cyprinus ca	1208	276	20.1	271	1	S24D ANOGA	Q17004 anopheles g
1136	283	20.6	247	1	TRXP SIMVI	P35048 simulium vi	1209	276	20.1	300	2	Q706U1	Q7q6u1 anopheles g
1137	283	20.6	320	2	Q7QKL3	Q7qkl3 anopheles g	1210	276	20.1	302	2	Q9VCJ0	Q9vcj0 drosophila
1138	283	20.6	382	2	Q76HL1	Q76hl1 mus musculus	1211	276	20.1	376	1	FA10_HOPST	P83370 hoptoccephal
1139	282.5	20.6	245	2	Q7PJQ0	Q7pjq0 anopheles g	1212	276	20.1	488	1	FA10_HUMAN	P00742 homo sapien
1140	282.5	20.6	246	2	Q817P0	Q817p0 lumbricus b	1213	276	20.1	717	2	Q8AKR1	Q8akr1 xenopus lae
1141	282.5	20.6	267	2	Q9VLF5	Q9vlf5 drosophila	1214	275.5	20.1	246	2	Q6DKQ2	Q6dkq2 eisenia foe
1142	282.5	20.6	269	2	Q9V929	Q9v929 drosophila	1215	275.5	20.1	249	2	Q8C1O8	Q8c1q8 mus musculus
1143	282.5	20.6	424	2	Q6RS58	Q6rs58 ostrinia nu	1216	275.5	20.1	256	2	Q818E5	Q818e5 ochlerotatu
1144	282.5	20.6	687	2	Q69DK8	Q69dk8 sus scrofa	1217	275.5	20.1	258	2	Q6NLM5	Q6nlm5 drosophila
1145	282	20.5	258	2	Q6JKF3	Q6jklf3 neodiprion	1218	275.5	20.1	262	2	Q9V5X9	Q9v5x9 drosophila
1146	282	20.5	259	2	Q18600	O18600 drosophila	1219	275.5	20.1	296	2	Q8T9U6	Q8t9u6 aedes aegypt
1147	282	20.5	263	2	Q9NB92	Q9nb92 agrotis ips	1220	275	20.0	237	2	Q17035	Q17035 anopheles g
1148	282	20.5	416	1	HEPS RAT	Q05511 rattus norv	1221	275	20.0	256	2	Q25082	Q25082 hypoderma l
1149	282	20.5	686	2	Q6Q1Q9	Q6q1q9 gallus gall	1222	275	20.0	260	2	Q9V5J1	Q9v5j1 drosophila
1150	282	20.5	688	2	Q868H4	Q868h4 branchiosto	1223	275	20.0	262	2	Q720G3	Q720g3 phlebotomus
1151	281.5	20.5	258	2	Q9NGY6	Q9ngy6 aedes aegypt	1224	275	20.0	284	2	Q8AXQ8	Q8axq8 xenopus lae
1152	281.5	20.5	291	2	Q8MLC5	Q8mlc5 drosophila	1225	275	20.0	317	2	Q7Q619	Q7q619 anopheles g
1153	281.5	20.5	388	2	Q7Z1F0	Q7z1f0 cotesia rub	1226	275	20.0	496	2	Q8CHP7	Q8chp7 cavia porce
1154	281.5	20.5	430	2	Q7PNQ4	Q7pnq4 anopheles g	1227	275	20.0	717	2	Q8AXR0	Q8axr0 xenopus lae
1155	281	20.5	262	2	Q720G5	Q720g5 phlebotomus	1228	274.5	20.0	695	1	CASP MESAU	P15156 mesocricetu
1156	281	20.5	267	2	Q9VA66	Q9va66 drosophila	1229	274	19.9	87	2	Q9CQ78	Q9cq78 m mus muscu
1157	281	20.5	329	2	Q7QB72	Q7qb72 anopheles g	1230	274	19.9	265	2	Q9VHF7	Q9vhf7 drosophila
1158	281	20.5	564	2	Q8MKB1	Q8mb1 oryctolagus	1231	273	19.9	125	2	Q86V18	Q86v18 homo sapien
1159	280.5	20.4	227	2	Q7PHB4	Q7phb4 anopheles g	1232	273	19.9	247	1	MCT8 MOUSE	P43430 mus musculus
1160	280.5	20.4	255	2	Q7Q100	Q7q100 anopheles d	1233	273	19.9	254	2	Q8K597	Q8k597 rattus norv
1161	280.5	20.4	270	2	Q7Q106	Q7q106 anopheles g	1234	273	19.9	257	2	Q818E3	Q818e3 aedes polyn
1162	280.5	20.4	365	2	Q9Y1K7	Q9y1k7 anopheles g	1235	273	19.9	258	1	TRVU DROER	P54629 drosophila
1163	280.5	20.4	410	2	Q7QJ44	Q7qj44 anopheles g	1236	273	19.9	265	2	Q17800	Q17800 caenorhabdi
1164	280.5	20.4	424	2	Q6RS59	Q6rs59 ostrinia nu	1237	273	19.9	288	2	Q9VEM8	Q9vem8 drosophila
1165	280.5	20.4	439	2	Q8BHM9	Q8bhm9 m mus muscu	1238	273	19.9	377	2	P79343	P79343 bos taurus
1166	280	20.4	241	1	Q7PQB3	Q7pqb3 anopheles g	1239	272.5	19.8	258	2	Q9GME1	Q9gme1 ornithorhyn
1167	280	20.4	254	1	TRYP_SARBU	P51588 sarcophaga	1240	272.5	19.8	262	1	TRVU DROME	P42279 drosophila
1168	280	20.4	267	2	Q8SYK8	Q8syk8 drosophila	1241	272.5	19.8	282	2	Q7FX30	Q7fx30 anopheles g
1169	280	20.4	271	2	Q9V4W5	Q9v4w5 drosophila	1242	272.5	19.8	287	2	Q9VTV2	Q9vtv2 drosophila
1170	280	20.4	282	2	Q25395	Q25395 lumbricus r	1243	272.5	19.8	432	1	UROK RAT	P22598 rattus norv
1171	280	20.4	336	2	Q7RTY5	Q7rty5 homo sapien	1244	272.5	19.8	537	2	Q804W8	Q804w8 fugu rubrip
1172	280	20.4	420	2	Q6IE14	Q6ie14 rattus norv	1245	272.5	19.8	978	2	P91777	P91777 pacifastacu
1173	280	20.4	494	2	Q9VUD7	Q9vjd7 drosophila	1246	272	19.8	243	2	O01310	O01310 botryllus s
1174	279.5	20.3	745	2	Q9PVY3	Q9pyv3 cyprinus ca	1247	272	19.8	262	1	TRVU DROME	P42278 drosophila
1175	279	20.3	242	2	Q6T374	Q6t374 eisenia foe	1248	272	19.8	262	2	Q9V5Y0	Q9v5y0 drosophila
1176	279	20.3	248	2	Q920S1	Q920s1 mus musculus	1249	272	19.8	288	2	Q8SX49	Q8sx49 drosophila
1177	279	20.3	267	2	Q9VA67	Q9va67 drosophila	1250	272	19.8	475	1	FA10 CHICK	P22155 gallus gall
1178	279	20.3	280	1	TRV2 DROME	P42280 drosophila	1251	272	19.8	492	2	Q7Z155	Q7z155 chitromantes
1179	279	20.3	280	2	Q9V5X8	Q9v5x8 drosophila	1252	272	19.8	688	1	C1S_HUMAN	P09871 homo sapien
1180	279	20.3	319	2	Q9VRS5	Q9vrs5 drosophila	1253	272	19.8	688	2	Q8CFG8	Q8cf8 mus musculus
1181	279	20.3	329	2	Q9GL10	Q9gl10 ovis aries	1254	271.5	19.8	250	2	Q7PWE3	Q7pwe3 anopheles g
1182	279	20.3	385	2	Q25101	Q25101 hermania m	1255	271.5	19.8	257	2	Q8IS83	Q8is83 aedes albop
1183	279	20.3	694	2	Q8R099	Q8r099 mus musculus	1256	271.5	19.8	262	2	Q9NB91	Q9nb91 agrotis ips
1184	279	20.3	694	2	Q6P6T1	Q6p6t1 rattus norv	1257	271.5	19.8	267	2	Q9V942	Q9v942 drosophila
1185	279	20.3	721	2	Q7ZT69	Q7zt69 lampetra ja	1258	271.5	19.8	272	2	Q9VRS3	Q9vrs3 drosophila
1186	278.5	20.3	269	2	Q7PWT2	Q7pwt2 anopheles g	1259	271.5	19.8	833	2	Q96442	Q96442 strongyloce
1187	278.5	20.3	326	2	Q7Z280	Q7z280 brachydanio	1260	271.5	19.8	247	2	Q70164	Q70164 mesocricetu
1188	278.5	20.3	330	2	Q6IE62	Q6ie62 rattus norv	1261	271	19.7	253	2	Q9XY50	Q9xy50 stenoccephal
1189	278.5	20.3	593	1	FA12 BOVIN	P98140 bos taurus	1262	271	19.7	275	2	Q7Z0B4	Q7z0b4 stomoxys ca
1190	278	20.2	239	2	Q9NKC5	Q9nkc5 drosophila	1263	271	19.7	1801	2	Q8WSJ2	Q8wsj2 bombyx mori
1191	278	20.2	474	2	Q7PZH7	Q7pzh7 anopheles g	1264	270.5	19.7	219	2	Q7PJ75	Q7pj75 anopheles g
1192	278	20.2	490	1	FA10_RABIT	O19045 oryctolagus	1265	270.5	19.7	245	2	Q6IE56	Q6ie56 rattus norv
1193	278	20.2	501	2	Q7QCVO	Q7qcv0 anopheles g	1266	270.5	19.7	248	1	GRAB_MOUSE	P11033 mus musculus
1194	277.5	20.2	245	2	Q9BLI8	Q9bli8 lumbricus r	1267	270.5	19.7	256	1	TRYB_MANSE	P35046 manduca sex
1195	277.5	20.2	266	2	Q24091	Q24091 drosophila	1268	270.5	19.7	420	2	Q7Q235	Q7q235 anopheles g
1196	277.5	20.2	271	2	Q76519	Q76519 stomoxys ca	1269	270	19.7	253	2	O18440	O18440 helicoverpa
1197	277.5	20.2	845	2	Q9DGR1	Q9dgr1 xenopus lae	1270	270	19.7	297	2	Q7Q6U4	Q7q6u4 anopheles g
1198	277	20.2	252	2	Q76498	Q76498 diaprepes a	1271	270	19.7	694	2	Q70542	Q70542 rattus norv
1199	277	20.2	272	2	Q82KG0	Q82kg0 streptomyce	1272	269.5	19.6	248	1	GR22_RAT	Q06606 rattus norv

1273	269.5	19.6	339	2	Q6BDA8	O6bda8 penaeus jap	1346	262	19.1	266	2	Q9VMX7	O9vmx7 drosophila
1274	269	19.6	235	2	Q9GTX7	Q9gtk7 aedes albop	1347	262	19.1	272	2	Q8SZG4	Q8szg4 drosophila
1275	269	19.6	244	2	Q8MMR5	Q8mrs5 dermatophag	1348	262	19.1	390	2	Q7PVQ3	Q7pvq3 anopheles g
1276	269	19.6	379	2	Q9NAS8	Q9na8 anopheles g	1349	262	19.1	427	2	Q7Q6T1	Q7q6t1 anopheles g
1277	269	19.6	389	2	Q7QGN4	Q7qgn4 anopheles g	1350	262	19.1	504	2	Q6PGW7	Q6pgw7 brachydanio
1278	269	19.6	445	2	Q7Q956	Q7q956 anopheles g	1351	261.5	19.0	259	2	O45048	O45048 anopheles g
1279	269	19.6	2616	1	NDL DROME	P8l159 drosophila	1352	261.5	19.0	262	2	Q7PX38	Q7px38 anopheles g
1280	268.5	19.5	245	2	Q6DF10	O6df10 xenopus tro	1353	261.5	19.0	297	2	Q7QNM1	Q7qnm1 anopheles g
1281	268.5	19.5	236	2	Q9Y842	Q9y842 metarhizium	1354	261.5	19.0	324	2	Q6BD08	Q6bd08 drosophila
1282	268.5	19.5	260	2	Q7Z0G4	Q7z0g4 phlebotomus	1355	261.5	19.0	366	2	Q7O170	Q7o170 mus musculus
1283	268.5	19.5	261	2	Q00344	Q00344 cochliobolu	1356	261.5	19.0	421	1	ACRO HUMAN	P10323 homo sapien
1284	268.5	19.5	262	1	TRYT DROER	P54628 drosophila	1357	261.5	19.0	669	2	Q7PWE1	Q7pwe1 anopheles g
1285	268.5	19.5	275	2	Q66UD0	O66ud0 culicoides	1358	261	19.0	239	2	P97595	P97595 rattus norv
1286	268.5	19.5	707	2	Q7OWK3	Q7owk3 oncorhynch	1359	261	19.0	246	2	P97611	P97611 rattus norv
1287	268	19.5	182	2	Q6PLJ6	O6plj6 penaeus jap	1360	261	19.0	262	2	Q7QFW4	Q7qfw4 anopheles g
1288	268	19.5	256	1	PRNJ HUMAN	P24158 homo sapien	1361	261	19.0	316	2	Q9VAQ2	Q9vaq2 drosophila
1289	268	19.5	270	2	Q9VKAG9	Q9vka9 drosophila	1362	260.5	19.0	242	1	FIBC LUMRU	P83298 lumbricus r
1290	268	19.5	277	2	Q6WN60	O6wn60 brachioosto	1363	260.5	19.0	242	2	O96687	O96687 eisenia foe
1291	267.5	19.5	249	2	Q6IB63	O6ieb63 rattus norv	1364	260.5	19.0	242	2	O8MX72	O8mx72 eisenia foe
1292	267.5	19.5	255	2	O44332	O44332 manduca sex	1365	260.5	19.0	242	2	O6T373	O6t373 eisenia foe
1293	267.5	19.5	280	2	Q6GLK1	O6gli1 xenopus lae	1366	260.5	19.0	245	2	Q7PFF6	Q7pff6 anopheles g
1294	267	19.4	182	2	Q6PLJ5	O6plj5 neocardina	1367	260.5	19.0	298	2	Q9VT25	Q9vt25 drosophila
1295	267	19.4	262	2	Q8SZQ7	O8szq7 drosophila	1368	260.5	19.0	264	2	Q7PE290	Q7pe290 anopheles g
1296	267	19.4	271	2	Q7PIA2	Q7pia2 anopheles g	1369	260.5	19.0	688	2	Q9PVI4	Q9pyv4 xenopus lae
1297	267	19.4	388	2	Q8I926	O8i926 hyphantria	1370	260	18.9	257	2	O8I8E2	O8i8e2 aedes trise
1298	266	19.4	222	2	Q7SIG2	Q7sig2 solenopsis	1371	260	18.9	282	2	Q7PVP7	Q7pvp7 anopheles g
1299	266	19.4	252	1	TRYI DROME	P52905 drosophila	1372	260	18.9	302	2	O8I1G9	O8i1g9 drosophila
1300	266	19.4	254	2	Q9XYT0	Q9xyt0 rhyzopertha	1373	259.5	18.9	252	2	O6I388	O6i388 mus musculus
1301	266	19.4	266	2	Q9VEM9	Q9vem9 drosophila	1374	259.5	18.9	275	2	Q66UHC	Q66uc8 culicoides
1302	266	19.4	273	2	Q8MTU7	O8mtu7 drosophila	1375	259.5	18.9	309	2	Q6DHH4	Q6dhh4 brachydanio
1303	266	19.4	277	2	Q8MLC4	O8mlc4 drosophila	1376	259.5	18.9	324	2	O6BD05	O6bd05 drosophila
1304	266	19.4	400	2	Q9GRG2	Q9grg2 tenebrio mo	1377	259.5	18.9	324	2	O6BD06	O6bd06 drosophila
1305	266	19.4	506	2	Q7PB64	Q7pb64 anopheles g	1378	259.5	18.9	324	2	O6BD16	O6bd16 drosophila
1306	265.5	19.3	322	2	Q6BD03	O6bd03 drosophila	1379	259.5	18.9	511	2	Q9VZH5	Q9vzh5 drosophila
1307	265.5	19.3	434	2	Q9V7S7	Q9v7s7 drosophila	1380	259.5	18.9	546	2	Q8SXG6	Q8sxg6 drosophila
1308	265.5	19.3	444	2	Q9V4W6	Q9v4w6 drosophila	1381	259	18.9	248	1	GRAE MOUSE	P08884 mus musculus
1309	265	19.3	251	2	Q9VQ99	Q9vq99 drosophila	1382	259	18.9	263	2	Q9V5X7	Q9v5x7 drosophila
1310	265	19.3	277	2	Q7QKR3	Q7qkr3 anopheles g	1383	259	18.9	279	2	Q7OE41	Q7qe41 anopheles g
1311	265	19.3	322	2	Q98G16	O98g16 rhizobium l	1384	258.5	18.8	167	2	O6URK9	O6urk9 bothrops ja
1312	265	19.3	415	1	ACRO FIG	P08001 sus scrofa	1385	258.5	18.8	248	2	O6IE58	O6ies8 rattus norv
1313	265	19.3	415	2	Q29015	Q29015 sus sp. pre	1386	258.5	18.8	285	2	O69997	O69997 streptomyce
1314	264.5	19.3	247	2	Q7PFF5	Q7pff5 anopheles g	1387	258.5	18.8	459	2	Q9V4W7	Q9v4w7 drosophila
1315	264.5	19.3	248	1	TRYF FUSOX	P35049 fusarium ox	1388	258.5	18.8	522	2	O8MQM9	O8mqm9 drosophila
1316	264.5	19.3	256	1	TRVA MANSE	P35045 manduca sex	1389	258.5	18.8	1089	2	O8T3A0	O8t3a0 ciona intes
1317	264.5	19.3	264	1	VDP BONMO	O07943 bombyx mori	1390	258	18.8	267	2	O9GP27	O9gp27 drosophila
1318	264.5	19.3	369	2	O6OE53	O6o53 callinectes	1391	258	18.8	269	2	Q7Q5I5	Q7q5i5 anopheles g
1319	264.5	19.3	719	2	Q9PVI2	Q9pvi2 triakis scy	1392	258	18.8	277	2	Q7Q595	Q7q595 anopheles g
1320	264	19.2	176	2	Q15098	Q15098 homo sapien	1393	258	18.8	295	2	O18445	O18445 helicoverpa
1321	264	19.2	180	2	Q96A30	Q96a30 homo sapien	1394	258	18.8	300	2	Q7Q6U0	Q7q6u0 anopheles g
1322	263.5	19.2	301	2	Q7PXG5	Q7pxg5 anopheles g	1395	258	18.8	352	2	Q7KVM3	Q7kvm3 drosophila
1323	263.5	19.2	251	1	CAP7 HUMAN	P20160 homo sapien	1396	258	18.8	387	2	Q7RTY4	Q7rty4 homo sapien
1324	263.5	19.2	256	2	O6R551	O6r551 ostrinia nu	1397	257.5	18.7	196	2	O6VFC8	O6vfc8 anopheles g
1325	263.5	19.2	258	2	Q9VMX9	Q9vmx9 drosophila	1398	257.5	18.7	248	2	O6IE09	O6ie09 rattus norv
1326	263.5	19.2	281	1	TRYZ DROER	P54630 drosophila	1399	257.5	18.7	254	2	Q01136	Q01136 metarhizium
1327	263.5	19.2	421	2	O6TCK2	O6tck2 homo sapien	1400	257.5	18.7	254	2	Q01136	Q01136 metarhizium
1328	263	19.1	180	2	O6T775	O6t775 homo sapien	1401	257.5	18.7	255	2	O97098	O97098 anopheles a
1329	263	19.1	241	2	Q7Q5E4	Q7q5e4 anopheles g	1402	257.5	18.7	259	2	O97097	O97097 anopheles a
1330	263	19.1	248	2	O8IRE2	O8ire2 drosophila	1403	257.5	18.7	274	2	O6DHC9	O6dhc9 brachydanio
1331	263	19.1	257	2	Q9VZT0	Q9vzt0 drosophila	1404	257.5	18.7	286	2	O96900	O96900 scolopendra
1332	263	19.1	272	2	Q7QIH5	Q7qih5 anopheles g	1405	257.5	18.7	326	2	Q7RTY6	Q7rty6 homo sapien
1333	263	19.1	289	2	Q945T9	Q945t9 phytothor	1406	257	18.7	237	2	Q6LBN2	Q6lbn2 homo sapien
1334	263	19.1	295	2	Q9N6C6	Q9n6c6 heliothis z	1407	257	18.7	256	2	O18441	O18441 helicoverpa
1335	263	19.1	300	2	O8IN70	O8in70 drosophila	1408	257	18.7	284	2	Q8MLV8	Q8mlv8 drosophila
1336	263	19.1	405	2	O8SZ60	O8sz60 drosophila	1409	257	18.7	417	2	O6JE90	O6je90 homo sapien
1337	263	19.1	467	2	O6IT09	O6it09 pseudonaja	1410	256.5	18.7	196	2	Q6VFD0	Q6vfd0 anopheles g
1338	262.5	19.1	256	1	TRYC MANSE	P35047 manduca sex	1411	256.5	18.7	235	1	TRYD HUMAN	Q9bdf3 homo sapien
1339	262.5	19.1	271	2	Q9VRS6	Q9vrs6 drosophila	1412	256.5	18.7	242	2	Q6NTB8	Q6ntb8 homo sapien
1340	262.5	19.1	281	2	O8SYB5	O8syb5 drosophila	1413	256.5	18.7	464	2	O9NK82	O9nk82 drosophila
1341	262.5	19.1	433	2	Q9QWF2	Q9qwf2 rattus sp.	1414	256	18.6	245	2	O9XY47	O9xy47 ctenocephal
1342	262.5	19.1	778	2	Q9V519	Q9v519 drosophila	1415	256	18.6	265	2	O9XY55	O9xy55 ctenocephal
1343	262	19.1	108	2	Q9CVU2	O9cvu2 mus musculus	1416	256	18.6	267	2	O9VRU0	O9vrU0 drosophila
1344	262	19.1	183	2	Q6PLJ7	O6plj7 femeropena	1417	256	18.6	282	2	Q7QCX2	Q7qcx2 anopheles g
1345	262	19.1	245	2	Q9VQ97	Q9vq97 drosophila	1418	256	18.6	403	2	Q9K5Q6	Q9ksq6 vibrio chol

1419	256	18.6	421	2	Q62MR5	Q6zmr5 homo sapien	1492	248	18.0	374	2	Q80YD5	Q80yd5 mus musculu
1420	256	18.6	463	2	Q6IT10	Q6it10 pseudonaja	1493	248	18.0	392	2	Q9VMZ3	Q9vmz3 drosophila
1421	255.5	18.6	220	2	Q6XI43	Q6xi43 drosophila	1494	248	18.0	401	2	Q6LHI7	Q6lhi7 photobacter
1422	255.5	18.6	254	2	Q18436	Q18436 helicoverpa	1495	247.5	18.0	260	2	Q9U4I4	Q9u4i4 plodia inte
1423	255.5	18.6	273	2	Q72163	Q72163 dermatophag	1496	247.5	18.0	291	2	Q6Y1Y9	Q6y1y9 lygus lineo
1424	255.5	18.6	431	2	Q7PV05	Q7pv05 anopheles g	1497	247	18.0	243	2	Q7M4I3	Q7m4i3 megabombus
1425	255	18.6	292	2	Q7PV05	Q7pvq5 anopheles g	1498	247	18.0	278	2	Q7Q8Q5	Q7q8q5 anopheles g
1426	255	18.6	405	2	Q7PNQ3	Q7pnq3 anopheles g	1499	247	18.0	350	2	Q9VCJ9	Q9vcj9 drosophila
1427	254.5	18.5	242	2	Q18434	Q18434 helicoverpa	1500	247	18.0	360	2	Q9WLX6	Q9wlx6 drosophila
1428	254.5	18.5	278	2	P91893	P91893 arenicola m							
1429	254.5	18.5	357	2	Q7Q092	Q7q092 anopheles g							
1430	254.5	18.5	357	2	Q7QXK6	Q7qxx6 anopheles g							
1431	254.5	18.5	493	2	Q7PV62	Q7pv62 anopheles g							
1432	254.5	18.5	523	2	Q9V819	Q9v819 drosophila							
1433	254.5	18.5	524	2	Q8MR00	Q8mr00 drosophila							
1434	254.5	18.5	827	2	Q7P288	Q7p288 anopheles g							
1435	254	18.5	324	2	Q6BD11	Q6bd11 drosophila							
1436	254	18.5	334	2	Q9VEA0	Q9vea0 drosophila							
1437	253.5	18.4	282	2	Q641D4	Q641d4 anthonomus							
1438	253	18.4	242	2	Q9XY59	Q9xy59 ctenocephal							
1439	253	18.4	251	2	Q9VXC9	Q9vxc9 drosophila							
1440	253	18.4	253	2	Q6W741	Q6w741 pediculus h							
1441	253	18.4	272	1	SER3 DROME	P17207 drosophila							
1442	253	18.4	287	2	Q675S0	Q675s0 oikopleura							
1443	252.5	18.4	245	2	Q7Q2Q8	Q7q2q8 anopheles g							
1444	252.5	18.4	254	2	Q76954	Q76954 lacanobia o							
1445	252.5	18.4	282	2	Q8MJD1	Q8mjd1 canis famil							
1446	252.5	18.4	324	2	Q6BD09	Q6bd09 drosophila							
1447	252	18.3	235	2	Q7PRK6	Q7prk6 anopheles g							
1448	252	18.3	295	2	Q18450	Q18450 helicoverpa							
1449	252	18.3	301	2	Q7Q6T0	Q7q6t0 anopheles g							
1450	252	18.3	400	2	Q27081	Q27081 tachypneus							
1451	251.5	18.3	186	2	Q6X655	Q6x655 marmota mon							
1452	251.5	18.3	266	2	Q8MLC2	Q8mlc2 drosophila							
1453	251.5	18.3	267	2	Q9VGB8	Q9vgb8 drosophila							
1454	251.5	18.3	276	2	Q18443	Q18443 helicoverpa							
1455	251.5	18.3	318	2	Q7QC37	Q7qc37 anopheles g							
1456	251.5	18.3	418	2	Q7Q529	Q7q529 anopheles g							
1457	251.5	18.3	520	2	Q8ING0	Q8ing0 drosophila							
1458	251	18.3	285	2	Q7Q5K4	Q7q5k4 anopheles g							
1459	251	18.3	405	2	Q8MQS8	Q8mq8 apis mellif							
1460	250.5	18.2	226	2	Q6XH04	Q6xhu4 drosophila							
1461	250.5	18.2	240	2	Q7PVJ1	Q7pvj1 anopheles g							
1462	250.5	18.2	268	2	Q9V724	Q9v724 drosophila							
1463	250.5	18.2	305	2	Q8MR12	Q8mr12 drosophila							
1464	250.5	18.2	323	2	Q76920	Q76920 drosophila							
1465	250	18.2	124	2	Q8CG55	Q8c855 mus musculu							
1466	250	18.2	258	2	Q9NB77	Q9nb77 heliothis z							
1467	250	18.2	258	2	Q9VSR6	Q9v86 drosophila							
1468	250	18.2	274	2	Q8MUG0	Q8mug0 glossina fu							
1469	249.5	18.2	253	2	Q18442	Q18442 helicoverpa							
1470	249.5	18.2	254	2	Q18447	Q18447 helicoverpa							
1471	249.5	18.2	258	2	Q7Q2P0	Q7q2p0 anopheles g							
1472	249.5	18.2	289	2	Q7PM15	Q7pm15 anopheles g							
1473	249.5	18.2	274	2	Q9VRS7	Q9vrs7 drosophila							
1474	249.5	18.2	282	2	Q18655	Q18655 plodia inte							
1475	249.5	18.2	327	2	Q8MS77	Q8ms77 drosophila							
1476	249.5	18.2	362	2	Q6LU71	Q6lu71 photobacter							
1477	249.5	18.2	520	2	Q8SY93	Q8sy93 drosophila							
1478	249	18.1	253	2	Q9NGY5	Q9ngy5 heliothis v							
1479	249	18.1	305	2	Q7Q6S4	Q7q6s4 anopheles g							
1480	249	18.1	388	2	Q966V2	Q966v2 halocynthia							
1481	249	18.1	714	2	Q7PWE5	Q7pwe5 anopheles g							
1482	248.5	18.1	296	2	Q9I711	Q9i711 drosophila							
1483	248.5	18.1	381	2	Q8MQY4	Q8mqy4 drosophila							
1484	248.5	18.1	746	2	O01654	O01654 halocynthia							
1485	248	18.0	141	2	Q6GKZ6	Q6gkz6 drosophila							
1486	248	18.0	257	2	Q8I1749	Q8i1749 pyrocoelia							
1487	248	18.0	257	2	Q945U0	Q945u0 phycophthor							
1488	248	18.0	258	2	Q9VZS9	Q9vzs9 drosophila							
1489	248	18.0	277	2	Q7Q141	Q7q141 anopheles g							
1490	248	18.0	277	2	Q7QNM2	Q7qnm2 anopheles g							
1491	248	18.0	367	2	Q7O169	Q7o169 mus musculu							

## ALIGNMENTS

## RESULT 1

ID	KLKC_HUMAN	STANDARD;	PRT;	248 AA.
AC	Q9UKR0; Q9UKR1;			
DT	16-OCT-2001 (Rel. 40, Created)			
DT	16-OCT-2001 (Rel. 40, Last sequence update)			
DT	25-OCT-2004 (Rel. 45, Last annotation update)			
DE	Kallikrein 12 precursor (EC 3.4.21.-) (Kallikrein-like protein 5)			
DE	(KLK-L5) (UNQ669/PRO1303).			
GN	Names=KLK12; Synonyms=KLK15;			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A. (ISOFORM 1).			
RX	MEDLINE=20118156; PubMed=10652563;			
RA	Yousef G.M., Luo L.-Y., Diamandis E.P.;			
RT	"Identification of novel human kallikrein-like genes on chromosome			
RT	19q13.3-q13.4.";			
RL	Anticancer Res. 19:2843-2852(1999).			
RN	[2]			
RP	SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).			
RA	Yousef G.M., Magklara A., Scorilas A., Diamandis E.P.;			
RT	"Cloning of new alternatively spliced forms of the kallikrein-like			
RT	gene 5 (KLK-L5).";			
RL	Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.			
RN	[3]			
RP	SEQUENCE FROM N.A. (ISOFORM 1).			
RX	PubMed=11054574; DOI=10.1016/S0378-1119(00)00382-6;			
RA	Can L., Lee I., Smith R., Argonza-Barrett R., Lei H., McCuaig J.,			
RA	Moss P., Paepfer B., Wang K.;			
RT	"Sequencing and expression analysis of the serine protease gene			
RT	cluster located in chromosome 19q13 region.";			
RL	Gene 257:119-130(2000).			
RN	[4]			
RP	SEQUENCE FROM N.A. (ISOFORM 1).			
RX	MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;			
RA	Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brueh J.,			
RA	Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,			
RA	Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,			
RA	Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,			
RA	Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,			
RA	Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,			
RA	Vandlen R., Watanabe C., Wicand D., Woods K., Xie M.-H., Yansura D.,			
RA	Xi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,			
RA	Godowski P., Gray A.;			
RT	"The secreted protein discovery initiative (SPDI), a large-scale			
RT	effort to identify novel human secreted and transmembrane proteins: a			
RT	bioinformatics assessment.";			
RL	Genome Res. 13:2265-2270(2003).			
RN	[5]			
RP	SEQUENCE FROM N.A.			
RX	PubMed=15057824; DOI=10.1038/nature02399;			
RA	Grimwood J., Gordon L.A., Olsen A.S., Terry A., Schmutz J.,			
RA	Lamerdin J.E., Hellsten U., Goodstein D., Couronne O., Tran-Gyamfi M.,			
RA	Aerts A., Altherr M., Ashworth L., Bajorek E., Black S., Branscomb E.,			
RA	Caenepeel S., Carrano A.V., Caolle C., Chan Y.M., Christensen M.,			
RA	Cleland C.A., Copeland A., Dalin E., Dehal P., Denys M., Dettler J.C.,			

RA Escobar J., Flowers D., Fotopoulos D., Garcia C., Georgescu A.M.,  
RA Glavina T., Gomez M., Gonzales E., Groza M., Hammon N., Hawkins T.,  
RA Haydu L., Ho I., Huang W., Israni S., Jett J., Kadner K., Kimball H.,  
RA Kobayashi A., Larionov V., Leem S.-H., Lopez F., Lou Y., Lowry S.,  
RA Malfatti S., Martinez D., McCreedy P.M., Medina C., Morgan J.,  
RA Nelson K., Nolan M., Ovcharenko I., Pitluck S., Pollard M.,  
RA Popkie A.P., Predki P., Quan G., Ramirez L., Rash S., Retterer J.,  
RA Rodriguez A., Rogers S., Salamov A., Salazar A., She X., Smith D.,  
RA Slezak T., Soloviyev V., Thayer N., Tice H., Tsai M., Ustaszewska A.,  
RA Vo N., Wagner M., Wheeler J., Wu K., Xie G., Yang J., Dubchak I.,  
RA Purey T.S., DeJong P., Dickson M., Gordon D., Eichler E.E.,  
RA Pennacchio L.A., Richardson P., Stubbs L., Rokhsar D.S., Myers R.M.,  
RA Rubin E.M., Lucas S.M.;  
RT "The DNA sequence and biology of human chromosome 19.";  
RL Nature 428:529-535(2004).  
CC -1- SUBCELLULAR LOCATION: Secreted (Probable).  
CC -1- ALTERNATIVE PRODUCTS:  
CC Event=Alternative splicing; Named isoforms=2;  
CC Name=1;  
CC IsoId=Q9UKR0-1; Sequence=Displayed;  
CC Name=2;  
CC IsoId=Q9UKR0-2; Sequence=VSP\_005403;  
CC -1- SIMILARITY: Belongs to the peptidase S1 family. Kallikrein  
CC subfamily.  
CC -----  
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CC -----  
DR ENBL; AF135025; AAD26426.2; -;  
DR ENBL; AF135025; AAF06065.1; -;  
DR ENBL; AF243527; AAG33365.1; -;  
DR ENBL; AY358524; AAQ88888.1; -;  
DR ENBL; AC011473; AAG23258.1; -;  
DR HSP; P00760; IEZX.  
DR MEROPS; S01.020; -;  
DR Gnew; HGNC:6360; KLIK2.  
DR MIM; 605539; -;  
DR GO; GO:0005576; C:extracellular; NAS.  
DR GO; GO:0004252; P:serine-type endopeptidase activity; NAS.  
DR GO; GO:0006508; P:proteolysis and peptidolysis; NAS.  
DR InterPro; IPR009003; Pept\_Ser\_Cys.  
DR InterPro; IPR001254; Peptidase\_S1.  
DR InterPro; IPR001314; Peptidase\_S1A.  
DR Pfam; PF00089; Trypsin; 1.  
DR PRINTS; PR00722; CHYMOTRYPSIN.  
DR SMART; SM00020; TRYPSIN\_DOM; 1.  
DR PROSITE; PS00240; TRYPSIN\_HIS; 1.  
DR PROSITE; PS00134; TRYPSIN\_HIS; 1.  
DR PROSITE; PS00135; TRYPSIN\_SER; 1.  
KW Alternative splicing; Glycoprotein; Hydrolase; Serine protease;  
KW Signal.  
FT SIGNAL 1 17 Potential.  
FT CHAIN 18 248 Kallikrein 12.  
FT ACT\_SITE 62 62 Charge relay system (By similarity).  
FT ACT\_SITE 108 108 Charge relay system (By similarity).  
FT ACT\_SITE 200 200 Charge relay system (By similarity).  
FT DISULFID 28 161 By similarity.  
FT DISULFID 47 63 By similarity.  
FT DISULFID 133 235 By similarity.  
FT DISULFID 140 206 By similarity.  
FT DISULFID 172 186 By similarity.  
FT DISULFID 196 222 By similarity.  
FT CARBOHYD 24 24 N-linked (GlcNAc...) (Potential).  
FT CARBOHYD 163 163 N-linked (GlcNAc...) (Potential).  
FT VARSPIC 236 248 KYVDWIRMIRNN -> NSFLVGLGTSWNFNSQCF (in  
FT isoform 2).  
FT /FTId=VSP\_005403.  
SQ SEQUENCE 248 AA; 26733 MW; BB473E98F8BAF703 CRC64;

Query Match 100.0%; Score 1374; DB 1; Length 248;  
Best Local Similarity 100.0%; Pred. No. 3.5e-102; Indels 0; Gaps 0;  
Matches 248; Conservative 0; Mismatches 0;  
QY 1 MGLSIFLLLCVLGLSQAATPKIFNGTECGRNQPMQVGLFEGTSLRCGGVLIDHRWLTA 60  
DB 1 MGLSIFLLLCVLGLSQAATPKIFNGTECGRNQPMQVGLFEGTSLRCGGVLIDHRWLTA 60  
QY 61 AHCSGRYVWRLGHEHLSOLDTEQIRHSGFSVTHPGYLGASTSHEDHLRLRLPVRV 120  
DB 61 AHCSGRYVWRLGHEHLSOLDTEQIRHSGFSVTHPGYLGASTSHEDHLRLRLPVRV 120  
QY 121 TSSVQPLPLPNDCATAGTCHVSGMGTNHPRPDQLQCLNLSIVSHATCHGVTPGRI 180  
DB 121 TSSVQPLPLPNDCATAGTCHVSGMGTNHPRPDQLQCLNLSIVSHATCHGVTPGRI 180  
QY 181 TSNMVCAGGVPQDQACQDGGGGLVCGVQLGIVSWGSGVPCQDGI PGVYTYCKYVDW 240  
DB 181 TSNMVCAGGVPQDQACQDGGGGLVCGVQLGIVSWGSGVPCQDGI PGVYTYCKYVDW 240  
QY 241 IRMIMERN 248  
DB 241 IRMIMERN 248  
RESULT 2  
Q9CV76 PRELIMINARY; PRT; 234 AA.  
ID Q9CV76 AC Q9CV76; DT 01-JUN-2001 (TrEMBLrel. 17, Created)  
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Mus musculus adult male tongue cDNA, RIKEN full-length enriched  
DE library, clone:2310008B01 product:similar to KALLIKREIN 12 (EC  
DE 3.4.21.-) (KALLIKREIN-LIKE PROTEIN 5) (KLK-L5) (Fragment).  
GN Name=Klik2;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Tongue;  
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;  
RA Carninci P., Hayashizaki Y.;  
RT "High-efficiency full-length cDNA cloning.";  
RL Meth. Enzymol. 303:19-44 (1999).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Tongue;  
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;  
RA RIKEN FANTOM Consortium;  
RT "Functional annotation of a full-length mouse cDNA collection.";  
RL Nature 409:685-690 (2001).  
RN [3]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Tongue;  
RA The FANTOM Consortium;  
RT "Analysis of the mouse transcriptome based on functional annotation of  
RT 60,770 full-length cDNAs.";  
RL Nature 420:563-573 (2002).  
RN [4]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Tongue;  
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;  
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,  
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;  
RT "Normalization and subtraction of cap-trapper-selected cDNAs to  
RT prepare full-length cDNA libraries for rapid discovery of new genes.";  
RL Genome Res. 10:1617-1630 (2000).  
RN [5]

```
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Tongue; DOI=10.1101/gr.152600;
RX MEDLINE=20530913; PubMed=11076861;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Kono H., Akiyama J., Nishi K., Kicsunai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.,
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer."
RL Genome Res. 10:1757-1771(2000).
RN [16]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Tongue;
RA Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
RA Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoaka T., Hori F.,
RA Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
RA Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
RA Matsuyana T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
RA Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
RA Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
RA Teijima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
RA Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to peptidase family S1.
DR EMBL; AK009217; BAB26143.1; -
DR HSSP; P00760; 1EZX.
DR MEROPS; S01.020; -.
DR MGD; MG1:1916761; Kklk12.
DR GO; GO:0004263; F:chymotrypsin activity; IEA.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004295; F:trypsin activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR0011254; Peptidase_S1.
DR InterPro; IPR0011314; Peptidase_S1.
DR InterPro; IPR009003; Pept_Ser_Cys.
DR Pfam; PF00089; Trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00020; TRYPSIN_1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Hydroxylase; Protease; Serine protease.
FT NON_TER 1
SQ SEQUENCE 234 AA; 25888 MW; 6D81E609EDD39110 CRC64;

Query Match 69.3%; Score 952.5; DB 2; Length 234;
Best Local Similarity 70.6%; Pred.No.1.9e-68;
Matches 166; Conservative 27; Mismatches 41; Indels 1; Gaps 1;

QY 14 LQAQAPPKIFNGTECGRNQPMQVGLFEGTSLRCGGVLIDHRWLVLPAAHCSGRYVRLG 73
DQ 1 LQAQDEKLYNGVECVKNSQPMQVGLFHGKLRCCGVLDKRWLVLPAAHCR-DKYVVRIG 59
QY 74 EHSLSOLDWTEQIRHSGFVTHPGYLGASTSHEDLRLRLPVRTSVSQVPLPNDG 133
DQ 60 EHSLTLDWTEQIRHSGFVTHPGYLGASTSHEDLRLRLPVRTSVSQVPLPNDG 119
QY 134 ATAGTECHVSGWGIVTHNRPDPDLQCLNLSVSHATGCVYVPGRTISNMVCAQGVPCQ 193
DQ 120 VTGAMCHVSGWGIVTHNRPDPDLQCLNLSVSHATGCVYVPGRTISNMVCAQGVPCQ 179
QY 194 DACQGDGSGGLVCGGVVQLGLVSGSVGPGCGQDGIPGVYTYICKYVDWIRMNRN 248
DQ 180 DACQGDGSGGLVCGGVVQLGLVSGSVGPGCGQDGIPGVYTYICKYVDWIRMNRN 234

RESULT 3
KLK8_HUMAN
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FT DISULFID 39 173 By similarity.
FT DISULFID 58 74 By similarity.
FT DISULFID 145 246 By similarity.
FT DISULFID 152 218 By similarity.
FT DISULFID 184 198 By similarity.
FT DISULFID 208 233 By similarity.
FT CARBOHYD 110 110 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 260 AA; 28510 MW; 58DF4F0602A0B7F5 CRC64;

Query Match 45.2%; Score 621.5; DB 1; Length 260;
Best Local Similarity 48.6%; Pred. No. 6.7e-42;
Matches 118; Conservative 32; Mismatches 90; Indels 3; Gaps 3;

QY 5 IFLL-CVLGLSQAATPKIFNGTEGRNSQPWQVGLFEGTSRCCGVLDHHRVLTAAHC 63
Db 15 LFLMGAGAGLTRAQGSKILEGQCKPHSQPWTALFQGERLVCGGVLDGRWLTAAHC 74

QY 64 SGRYVRLGHSLSQLDWTEQIRISGFSVTHPGVILGAS-TSHEHDLRLRLPLRVTS 122
Db 75 KDKYSVRLGDHSLQKRDPEQEIQVARSIQHPCFNSSNPEDHSHDMLRLQNSANLGD 134

QY 123 SVQPLPLPNDCATAGTECHVSGWGITNHPNFPDLOCLNLSIVSHATCHGVYGRITS 182
Db 135 KVKPIELANLCPKVGQKCIISGWITVSPQENFPNTLCAEVKIYSONKCEAYFGKITE 194

QY 183 NMVCGAGVPGDACQDGGGLVCGGVLLGLVSGVSGPGQDGPVYTYICKYVDWIR 242
Db 195 GNVCGAGSNGADTCQDGGGLVCGGVLLGLVSGVSGPGQDGPVYTYICKYVDWIR 253

QY 243 MTM 245
Db 254 KTM 256

RESULT 7
KLKB HUMAN STANDARD; PRT; 250 AA.
AC Q9UBX7; O75837; Q9NS65;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Kallikrein 11 precursor (EC 3.4.21.-) (Hippostasin) (Trypsin-like
DE protease) (UNQ649/PRO1279).
GN Name=KLK11; Synonyms=PRSS20, TLSP;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;

SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RC TISSUE=Testis;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon J.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- FUNCTION: Possible multifunctional protease. Efficiently cleaves
CC bz-Phe-Arg-4-methylcoumaryl-7-amide, a kallikrein substrate, and
CC weakly cleaves other substrates for kallikrein and trypsin.
CC -!- SUBCELLULAR LOCATION: Secreted.

SEQUENCE FROM N.A. (ISOFORM 1).
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RX PubMed=11054574; DOI=10.1016/S0378-1119(00)00382-6;
RA Gan L., Lee I., Smith R., Argonza-Barrett R., Lei H., McCuaig J.,
RA Moss P., Paepir B., Wang K.;
RT "Sequencing and expression analysis of the serine protease gene
RL cluster located in chromosome 19q13 region."
RN Gene 257:119-130(2000).

SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
RA Eaton D., Foster J., Grimaldi C., Gu Q., Hase P.E., Heldens S.,
RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,
RA Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
RA Vandlen R., Watanabe C., Wieand D., Woods K., Xie M.-H., Yansura D.,
RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
RA Godowski P., Gray A.;
RT "The secreted protein discovery initiative (SPDI), a large-scale
RT effort to identify novel human secreted and transmembrane proteins: a
RT bioinformatics assessment."
RN Genome Res. 13:2265-2270(2003).

SEQUENCE FROM N.A.
RX PubMed=15057824; DOI=10.1038/nature02399;
RA Grimwood J., Gordon L.A., Olsen A.S., Terry A., Schmutz J.,
RA Lamerdin J.E., Hellsten U., Goodstein D., Couronne O., Tran-Gyamfi M.,
RA Aerts A., Altherr M., Ashworth L., Bajorek E., Black S., Branscomb E.,
RA Caenepeel S., Carrano A.V., Caoile C., Chan Y.M., Christensen M.,
RA Cleland C.A., Copeland A., Dalin E., Dehal P., Denys M., Dettler J.C.,
RA Escobar J., Flowers D., Fotopulos D., Garcia C., Georgescu A.M.,
RA Glavina T., Gomez M., Gonzales E., Groza M., Hammon N., Hawkins T.,
RA Haydu L., Ho I., Huang W., Istrani S., Jett J., Kadner K., Kimball H.,
RA Kobayashi A., Larionov V., Leem S.-H., Lopez F., Lou Y., Lowry S.,
RA Malfatti S., Martinez D., McCready P.M., Medina C., Morgan J.,
RA Neilson K., Nolan M., Ovcharenko I., Fittluck S., Pollard M.,
RA Popkie A.P., Predki P., Qian G., Ramirez L., Rash S., Retterer J.,
RA Rodriguez A., Rogers S., Salamov A., Salazar A., She X., Smith D.,
RA Slezak T., Solovyev V., Thayer N., Tice H., Tsai M., Ustaszewska A.,
RA Vo N., Wagner M., Wheeler J., Wu K., Xie G., Yang J., Dubchak I.,
RA Pury T.S., DeJong P., Dickson M., Gordon D., Eichler E.E.,
RA Pennacchio L.A., Richardson P., Stubbs L., Rokhsar D.S., Myers R.M.,
RA Rubin E.M., Lucas S.M.;
RT "The DNA sequence and biology of human chromosome 19."
RN Nature 428:529-535(2004).

SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RC TISSUE=Testis;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon J.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- FUNCTION: Possible multifunctional protease. Efficiently cleaves
CC bz-Phe-Arg-4-methylcoumaryl-7-amide, a kallikrein substrate, and
CC weakly cleaves other substrates for kallikrein and trypsin.
CC -!- SUBCELLULAR LOCATION: Secreted.
```







"Molecular cloning of the human kallikrein 15 gene (KLK15). Up-regulation in prostate cancer.";  
J. Biol. Chem. 276:53-61(2001).  
[2]  
SEQUENCE FROM N.A.  
RX PubMed=11054574; DOI=10.1016/S0378-1119(00)00382-6;  
Gan L., Lee I., Smith R., Argonza-Barrett R., Lei H., McCuaig J., Moss P., Paepér B., Wang K.;  
RA "Sequencing and expression analysis of the serine protease gene cluster located in chromosome 19q13 region.";  
RT cluster located in chromosome 19q13 region.";  
RL Gene 257:119-130(2000).  
[3]  
PRELIMINARY PARTIAL SEQUENCE FROM N.A.  
RP TISSUE=Brain;  
RC MEDLINE=94289486; PubMed=8018728; DOI=10.1016/0167-4781(94)90018-3;  
RX Dihanich M.E., Spiess M.;  
RA "A novel serine protease-like sequence from human brain.";  
RT Biochim. Biophys. Acta 1218:223-228(1994).  
[4]  
SPLICE ISOFORM(S) THAT ARE POTENTIAL NMD TARGET(S).  
RP PubMed=14759258; DOI=10.1186/gb-2004-5-2-r8;  
RX Hillman R.T., Green R.E., Brenner S.E.;  
RA "An unappreciated role for RNA surveillance.";  
RL Genome Biol. 5:RESEARCH008.1-RESEARCH008.16(2004).  
CC -!- FUNCTION: Protease whose physiological substrate is not yet known.  
CC -!- SUBCELLULAR LOCATION: Secreted (Probable).  
CC -!- ALTERNATIVE PRODUCTS:  
CC Event=Alternative splicing; Named isoforms=4;  
CC Name=1;  
CC IsoId=Q9H2R5-1; Sequence=Displayed;  
CC Name=2;  
CC IsoId=Q9H2R5-2; Sequence=VSP\_005405;  
CC Note=May be produced at very low levels due to a premature stop codon in the mRNA, leading to nonsense-mediated mRNA decay;  
CC Name=3;  
CC IsoId=Q9H2R5-3; Sequence=VSP\_005406, VSP\_005407;  
CC Name=4;  
CC IsoId=Q9H2R5-4; Sequence=VSP\_005404;  
CC -!- TISSUE SPECIFICITY: Highest expression in the thyroid gland. Also expressed in the prostate, salivary, and adrenal glands and in the colon testis and kidney.  
CC -!- SIMILARITY: Belongs to the peptidase S1 family. Kallikrein subfamily.  
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DR EMBL; AF242195; AAG09469.1; --  
DR EMBL; AF242195; AAG09470.1; --  
DR EMBL; AF242195; AAG09471.1; --  
DR EMBL; AF242195; AAG09472.1; --  
DR EMBL; AF243527; AAG33354.1; --  
DR EMBL; X75363; CAA53145.1; ALT\_SEQ.  
DR HSSP; P00760; 1EXX.  
DR MEROPS; S01.081; --  
DR Genew; HGNC:20453; KLK15.  
DR GO; GO:0005576; C:extracellular; NAS.  
DR GO; GO:004252; F:serine-type endopeptidase activity; NAS.  
DR GO; GO:0006508; P:proteolysis and peptidolysis; NAS.  
DR InterPro; IPR009003; PeptSer\_Cys.  
DR InterPro; IPR001254; Peptidase\_S1.  
DR InterPro; IPR001314; Peptidase\_S1A.  
DR Pfam; PF00089; Trypsin; 1.  
DR PRINTS; PR00722; CHYMOTRYPSIN.  
DR SMART; SM00020; TRYPSIN\_DOM; 1.  
DR PROSITE; PS00240; TRYPSIN\_DOM; 1.  
DR PROSITE; PS00134; TRYPSIN\_HIS; 1.  
DR PROSITE; PS00135; TRYPSIN\_SER; FALSE\_NEG.

KW Alternative splicing; Glycoprotein; Hydrolase; Serine protease;  
KW SIGNAL; Zymogen.  
FT SIGNAL 1 16 Potential.  
FT PROPEP 17 21 Activation peptide (Potential).  
FT CHAIN 22 256 Kallikrein 15.  
FT ACT SITE 62 62 Charge relay system (By similarity).  
FT ACT SITE 106 106 Charge relay system (By similarity).  
FT ACT SITE 209 209 Charge relay system (By similarity).  
FT CARBOHYD 171 171 N-linked (GlcNAc...) (Potential).  
FT CARBOHYD 232 232 Missing (in isoform 4).  
FT VARSPLIC 122 206 /FTID=VSP\_005404.  
FT VARSPLIC 122 256 Missing (in isoform 2).  
FT VARSPLIC 161 161 /FTID=VSP\_005405.  
FT VARSPLIC 162 256 /FTID=VSP\_005406.  
FT VARSPLIC 162 256 Missing (in isoform 3).  
FT CONFLICT 147 160 SHNEFTAGSPRSQ -> PLSSP (in Ref. 2).  
SQ SEQUENCE 256 AA; 28087 MW; B5EBF8D6022786B5 CRC64;  
Query Match 43.6%; Score 599; DB 1; Length 256;  
Best Local Similarity 47.1%; Pred. No. 4.2e-40;  
Matches 121; Conservative 32; Mismatches 88; Indels 16; Gaps 6;  
QY 5 IFLLCVLGLSQAAT--PKIFNGTECRNSQWQVGLFEGTSLRCGVLIDHRWVLTAAH 62  
DB 3 LLLTLFLASTAAQDGKLLGDECAHQSQWQVGLYERGFNCGLSIPHWLSAAH 62  
QY 63 CSGSYWVRLGHSLSQLDWTEQIRHSGFVTHPGYLGASTSHEHDLRLRLPVRVTS 122  
DB 63 QSRPMRVRLGEHNLKRDGPQLRTTSRVIPHPRY--EARSHRNDIMLLRLVQPARLP 120  
QY 123 SVQPLPLNDCATAGTECHVSGWGITNH-----PRN--PFPLQLCLNLSIVSHATC 172  
DB 121 QVRPAVLPTCRPHGAEACVSGWGLVSHNEPOTAGSPRSQVSLPDTLHLCANISLSDTSC 180  
QY 173 HGVPGRITSNMVCAGGV-PGQDACQSGSGPLVCGVGLQGLVSGVSPCCQDGPVGVY 231  
DB 181 DKSYPGLTNTMVCAGAEGRGAESCEGDSGLVCGVGLQGLVSGVSPCCQDGPVGVY 239  
QY 232 TVICKYVDWIRMIMRN 248  
DB 240 TKVCHYLEWIRETMKRN 256  
RESULT 14  
Q9QYN4 PRELIMINARY; PRT; 249 AA.  
AC Q9QYN4;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Hippocasin.  
GN Name=2310015108Rik;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Brain;  
RX MEDLINE=20525460; PubMed=11072088; DOI=10.1016/S0167-4781(00)00206-2;  
RA Mitsui S., Okui A., Kominami K., Uemura H., Yamaguchi N.;  
RT "cDNA cloning and tissue-specific splicing variants of mouse hippocasin/TLSP (PRSS20).";  
RL Biochim. Biophys. Acta 1494:206-210(2000).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Brain;  
RA Yamaguchi N., Mitsui S.;  
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.  
CC -!- SIMILARITY: Belongs to peptidase family S1.

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DR EMBL; AB016226; BAA88825.1; -.
DR HSP; P00760; 1EZX.
DR MEROPS; S01_257; -.
DR MGD; MGI:1929977; 2310015108rik.
DR GO; GO:0005615; C:extracellular space; TAS.
DR InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR InterPro; IPR009003; Pept_Ser_Cys.
DR Pfam; PF00089; Trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00020; Tryp_Spc; 1.
DR PROSITE; PS02240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Hydrolase; Protease; Serine protease.
SQ SEQUENCE 249 AA; 27604 MW; F9FP9CB457D727D5 CRC64;

Query Match 43.5%; Score 597.5; DB 2; Length 249;
Best Local Similarity 47.0%; Pred. No. 5.4e-40;
Matches 118; Conservative 33; Mismatches 95; Indels 5; Gaps 4;

QY 1 MGLSIFLLCVLGLSQAATPKIENGTECGNSQPWQVGLFEGTSLRCGGVLDHRWVLTFA 60
Db 1 MIURLIALVTHVGGET-RIITGYECRPHSQPQWQVALFQKRLCCGATLAPKWLTA 59

QY 61 AHCSGRYVWRLGEHSLQDLWTEQIRHSGFVTHPGYLGA--STSHEDLRLRLRLPV 118
Db 60 AHCRKPHYVLLGEHNLKTDGCEQRMRATESFPHPDFNNSLPNKRDRNDMLVQMSPPV 119

QY 119 RVTSSVQPLPLPNDCTAGTECHVSGWGTNHPNRPFPDLLOCLNLSIVSHATCHGVYPG 178
Db 120 FETRAVQPLTSLPHCAAGTSCLLISGWGTTSSPQLRLPHSLRCANVSIIEHKECEKAYPG 179

QY 179 RITSNMVACAG-GVPGODACGSGGLVCGVGLQGLVSGVSGPCQDGIQGVVYICKY 237
Db 180 NITDTWLCASVRKXGDKSCGSGGLVCGVGLQGLISWQGDPCAVTRKPGVYTKVCKY 238

QY 238 VDWMIRMNRRN 248
Db 239 FNNIHEVMNRRN 249

RESULT 15
Q9QYN3 PRELIMINARY; PRT; 276 AA.
AC Q9QYN3;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hippocastin prostate type (Mus musculus adult male tongue cDNA, RIKEN full-length enriched library, clone:2310015108 product:protease, serine, 20, full insert sequence) (Mus musculus adult male tongue cDNA, RIKEN full-length enriched library, clone:2310040F07 product:protease, serine, 20, full insert sequence).
GN Name=2310015108rik;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Prostate;
RX MEDLINE=20525460; PubMed=11072088; DOI=10.1016/S0167-4781(00)00206-2;
RA Mitsui S., Okui A., Kominami K., Uemura H., Yamaguchi N.;
RT "cDNA cloning and tissue-specific splicing variants of mouse hippocastin/TLSP (PRSS20).";
RL Biochim. Biophys. Acta 1494:206-210 (2000).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Prostate;
RA Yamaguchi N., Mitsui S.;
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
RN [3]

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RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Tongue;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44 (1999).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Tongue;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690 (2001).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Tongue;
RA The FANTOM Consortium;
RT "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";
RL Nature 420:563-573 (2002).
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Tongue;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630 (2000).
RN [7]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Tongue;
RX MEDLINE=20530913; PubMed=11078661; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoaka S., Sasaki N., Carninci P., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771 (2000).
RN [8]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Tongue;
RA Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H., Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M., Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F., Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H., Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C., Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M., Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K., Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T., Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T., Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M., Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to peptidase family S1.
DR EMBL; AB016227; BAA36955.1; -.
DR EMBL; AK009360; BAB26241.2; -.
DR HSP; P00760; 1EZX.
DR MEROPS; S01_257; -.
DR MGD; MGI:1929977; 2310015108rik.
DR GO; GO:0005615; C:extracellular space; TAS.
DR InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR InterPro; IPR009003; Pept_Ser_Cys.
DR Pfam; PF00089; Trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00020; Tryp_Spc; 1.

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